111104, A 6417, Ap 8134, Ap 6468, Ap 7404, Ap 8132, Ap 3, Appli 6899, Ap

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June 7, 2005, 14:02:07; Search time 43 Seconds (without alignments) 694.410 Million cell updates/sec
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2029
1 MGLGNGRRSMKSPPLVLAAL......DQKRDTINLLDQREKRNHTL
version 5.1.6
- 2005 Compugen Ltd
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                                                                      protein search, using sw model
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GenCore (c) 1993
                 Copyright
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Issued Patents AA:*

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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

seq length: 0 seq length: 2000000000

Minimum DB Maximum DB

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

94, Appl 94, Appl 1280, Ap 10872, A 863, App 6611, Ap 11417, A 5756, Ap 15753, A 918, App Sequence 202, App Sequence 357, App Sequence 389, App Description Sequence Sequence Sequence Sequence Sequence 1 Sequence 5 Sequence US-09-489-847-352 US-09-673-395A-389 US-09-538-092-911 US-09-949-016-8888 US-08-866-108A-15754 US-08-800-644-94 US-09-538-092-1280 US-09-538-092-1280 US-09-538-092-1280 US-09-549-016-10872 US-09-949-016-10872 US-09-949-016-6611 US-09-949-016-6611 US-09-949-016-6611 US-09-949-016-6611 US-09-949-016-6611 US-09-949-016-6611 US-09-949-016-11877 US-09-949-016-7646 US-09-949-016-7646 US-09-949-016-7646 US-09-949-016-7646 US-09-949-016-7647 US-09-949-016-7647 US-08-949-016-7647 Length 3878 119940 115863 118898 118898 118898 118898 11898 1 Query 2020 2020 631 168 166.5 166.5 165.5 165.1 160.5 160.5 160.5 160.5 188.5 158.5 158.5 157.5 1157.5 1157.5 1157.5 1157.5 1157.5 1157.5 1157.5 1157.5 Result

47, Ap Appli Appli

Sequence Sequence Sequence Sequence , Sequence Sequence Sequence

Appli

US-08-483-924-4 US-09-452-294-1 PCT-US93-06160-4

NAME/KEY: SITE

1. LOCATION: (307)

2. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-489-847-202 1271, Ap 2, Appli 2, Appli 2, Appli 2, Appli 10828, A DQLKTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKG 180 9 61 Sequence 915, App Sequence 11104, Sequence 81134, App Sequence 6468, App Sequence 6468, App Sequence 8135, App Sequence 3, Appl, Sequence 6925, Applence 6925, Applence 1311, Applence 6925, Applence 1311, Applence 1311, Applence 1311, Applence 2111, Applence 211 2 MGLGNGRRSMKSPPLVLAALVACIIVLGFNYMIASSRSVDLQTRIMELEGRVRRRAAERG 1 MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG Sequence Sequence Sequence Sequence ö 99.6%; Score 2020; DB 4; Length 401; 99.5%; Pred. No. 2e-163; ive 0; Mismatches 2; Indels US-09-538-092-915
US-09-949-016-11104
US-09-949-016-6417
US-09-949-016-6468
US-09-949-016-6468
US-09-949-016-6468
US-09-949-016-6468
US-09-949-016-6899
US-09-949-016-6899
US-09-949-016-6925
US-09-538-092-1271
US-09-538-092-1271
US-09-538-092-1271
US-09-298-568-2
US-09-949-016-10828 TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: P2031P1
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER PILING DATE: 1998-08-06
SARLIER PILING DATE: 1998-08-06
SARLIER PILING DATE: 1998-08-06
SOFTWARE: PALENTIN VOWER: 60/095,455
SOFTWARE: PALENTIN VOWER: 60/095,455
SOFTWARE: PALENTIN VOWER: 00/095,455
SOFTWARE: PALENTIN VOWER: 00/095,455
SOFTWARE: PALENTIN VOWER: 00/095,455 ALIGNMENTS Sequence 202, Application US/09489847 Patent No. 6476195 GENERAL INFORMATION: Best Local Similarity 99.5 Matches 398; Conservative 1933 11933 11953 11953 11962 11780 11780 1162 11162 11162 11162 ORGANISM: Homo sapiens US-09-489-847-202 157 156.5 156.5 156.5 156.5 157.5 153.5 153.5 153.5 151.5 151.5 151.5 151.5 151.5 61 62 121 122 Query Match 셤 q g ઠ ઠ ∙&

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                                                                         339 RNQQKLRGEDDYNMDENEAESETDKQAALAGNDRNIDVFNVEDQKRDTINLLDQREKRNH 398
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APPLICANT: SPECHT, THOMAS
APPLICANT: SCHMITT, ARMIN
APPLICANT: SCHMITT, ARMIN
APPLICANT: SCHMITT, ARMIN
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: DAHL, EDGAR
APPLICANT: DAHL, EDGAR
APPLICANT: ROSENTHAL, ANDRE
TITLE OF INVENTACIN: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
FILE REFERENCE: ALBRE-12
CURRENT FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 637
SOFTWARE: PATCHIN VOE: 2.1
SEQ ID NO 389
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Best Local Similarity 100.0%; Pred. No. 4.8e-46;
Matches 122; Conservative 0; Mismatches 0; Indels
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APPLICANT: MINERANION:
APPLICANT: Mylliams, Mark
ITLIE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES; FILE REFERENCE: 8471-010-999; CURRENT APPLICATION NUMBER: US/09/914,259; CURRENT PILING DATE: 2000-11-21; NUMBER OF SEQ ID NOS: 180; SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                       361 TDKQAALAGNDRNIDVFNVEDQKRDTINLLDQREKRNHTL 400
                                                                                                                                                            383 TDKQAALAGNDRNIDVFNVEDQKRDTINLLDQREKRNHTL 422
                                                                                                                                                                                                                                                                                   ; Sequence 389, Application US/09673395A; Patent No. 6620923; GENERAL INFORMATION:
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CRGANISM: Homo sapiens
US-09-914-259-11
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US-09-673-395A-389
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TL 148
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LOCATION: (328)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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         NEAVASRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSE 240
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                                                                                                                     242 VVLDSKRQVEKEETNEIOVVNEEPORDRLPQEPGREGVVEDRPVGGRGFGGAGELGGTPO 301
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                                       182 NEAVASRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSE
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                                                                                                                                                                                                                                                                                               TDKQAALAGNDRNIDVFNVEDQKRDTINLLDQREKRNHTL 401
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APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: P2031P1
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1998-07-30
EARLIER FILING DATE: 1998-07-30
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
SARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER: OF SEQ ID NOS: 376
SOFTWARE: PETENT VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 357, Application US/09489847
Patent No. 6476195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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; ORGANISM: Human
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                                                                                                                       3212 ELEDLKFSLESOKORNLOLNLLLEQOKOLLNESOOKİE----SORMLYDAOLSEEOGRN 3266
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                                                      1230 DDLSSSME-SVSKSKANLEKICRTLEDQLSEARGKNEE--IQRSLSELTTQKSRLQTEAG 1286
                                                                                                  83 IQSSHNFQLESVN---KLYQDEKAVLVNNITTGERLIRVLQDQLKTLQRNYGRLQQ---D 136
                                                                                                                                                                   137 VLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRDLSENNDQR 196
                                                                                                                                                                                                                                    QQLQALSEPQP----RLQAAGLP-----HTEVPQGKGNVLGNSKSQTPAPSSEVVLDSKRQ 248
                                                                                                                                                                                                                                                                                                       VEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVS 308
                                                                                                                                                                                                                                                                                                                                                                          QENPEMEGPERD---QLVIPDGQEEEQEAAGEGRNQQXLRG-EDDYNMDENEAESETDKQ 364
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                                 26 VLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERGAVELKKNEFQGELEKQREQLD---K
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APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/127,365
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 901
     44; Gaps
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; OTHER INFORMATION: Polypeptide Accession Number P11055
US-09-538-092-901
 Mismatches 158;
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Patent No. 6753314
GENERAL INFORMATION:
 90;
74; Conservative
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ORGANISM: Homo sapiens
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US-09-538-092-901
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# PACELIA INCOMATION:
# CERERAL INCOMATION:
# APPLICANT: VENTER, J. Craig et al.
# TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
# TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
# FILE REPERENCE: CL001307
# CURRENT APPLICATION NUMBER: US/09/949,016
# PRIOR APPLICATION NUMBER: 60/241,755
# PRIOR PILING DATE: 2000-10-20
# PRIOR PILING DATE: 2000-10-30
# PRIOR PILING DATE: 2000-10-30
# PRIOR PILING DATE: 2000-09-08
# NUMBER: 60/231,498
# PRIOR FILING DATE: 2000-09-08
# NUMBER: OF SEQ ID NOS: 207012
# NUMBER: PRESEQ FOR Windows Version 4.0
                                                  1287 ELSR-----QLEEKESIVSQLSRSKQAFTQQTEEL----KRQLE-EENKAKNALAHAL 1334
                                                                                                                                                                                                                                                                                        | :: |: :|: :|: || 193 AEFLKLRRDLGEATLQHEAWVATLRKKHADSVAELGEQIDNLQRVKQKLEKEKSEFKLEI 1252
                                                                                                                                                                                       1335 ÖSSÄHDCDLLREÖYEEEQE-----GKAEL-----QRALSKANSEVAQWRTKYETDAI 1381
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                                                                                                                                                                                                                                                       QENPEMEGPERDQLVIPDGQEEEQEA----AGEGRNQQKLRGE-DDYNMDENEAESETD 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 DEKAVLVNNITTG----ERLIRVLQ-----DQLKTLQRNYGRLQQDVLQFQKNQ 144
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                                                                                                                        ORDRIPOEPGREOVVEDRPVGGRGFGGAGELGOTPOVOAALSVS----
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; Pred. No. 5.7e-05;
61; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8888, Application US/09949016
; Patent No. 6812339
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Similarity 23.9%;
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Best Local Similarity 23...
Lag 89; Conservative (
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SOFTWARE: Patentin Release #1.0, VerCURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/056,200
FILING DATE: 30-APR-1993
CLASSIFFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NHOS4.0011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    ; Sequence 94, Application US/08056200
; Patent No. 5616500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1898 amino acids
                                                                                                                                                                                                                                                                                                                       APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, Soo-Il
APPLICANT: Park, Sang-Chul
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                   APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKG
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22.9%; Pred. No. 5.1e-05;
ive 67; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR PELLING DATE: 2001-09-29
PRIOR PELLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-07
PRIOR PELLING DATE: 2000-01-07
PRIOR PLING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 15755
                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Aeomica Sequence Listing Engine
                                                                                                         Sequence 15754, Application US/09866108A
1462 LAAALDKKORNFD 1474
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; ORGANISM: Homo sapiens
US-09-866-108A-15754
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Best Local S:
Matches 96
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291 GAGELGQTPQVQAALSVSQENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDY 350
                                                                                                                                     GLPHTEVPQGKGNVLGNSKSQTPAPSSEVVLDSKRQVEKEFINEIQVVNEEPQRDRLPQ- 271
                                                                                                       351 NMDENEAESET------DKQAALAG---NDRNIDVFNVEDQKRDTINLLDQR 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and TITLE OF INVENTION: Mehods of Using Same NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
8.1%; Score 165; DB 1; Length 1898;
Best Local Similarity 23.2%; Pred. No. 7.3e-05;
Matches 89; Conservative 71; Mismatches 133; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
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635 --RDERLKREEPEEERRHELLKSEEQEERRHEQLRRE--QQERREQRLKREEEEERLEQR 690
EGRVRRAAAERGAVELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNN 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 INOMKEVKEQCEERIEEVTKKGNEAVASR-----DLSENNDORQOLQALSEPQPRLQAA 212
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                                                                                          GLPHTEVPQGKGNVLGNSKSQTPAPSSEVVLDSKRQVEKEETNEIQVVNEEPQRDRLPQ- 271
                                                                                                                              -----EPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQENPEMEGPERDQLVIP 325
                                                                                                                                                                                                                                                               790 QABEKSERGKQRLSARPPLREQ-----RERQLRAE-----ERQQREQRFLP 830
                                                                                                                                                                                                                                                                                                                        DGQEEEQEAAGEGRNQ-----QXLRGEDDYNMDENEAESETDKQAALAGNDRNIDVFNVE 380
                                                                                                                                                                                                                                                                                                                                                      213 GLPHTEVPQGKGNVLGNSKSQTPAPSSEVVLDSKRQVEKEETNEIQVVNEEPQRDRLPQ- 271
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APPLICANT: Manafield, Traci A.
APPLICANT: Manafield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: 60/127,352
FRIOR PRILING DATE: 1999-04-01
FRIOR PILING DATE: 1999-04-01
FRIOR PILING DATE: 1000-02-01
NUMBER OF SEC ID NOS: 1387
SOFTWARE: CLIAPALSeqFormatter Version 0.9
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23.2%; Pred. No. 7.3e-05;
tive 71; Mismatches 133; Indels
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, TOTHER INFORMATION: Polypeptide Accession Number Q07283
US-09-538-092-1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1280, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        DOKRD ---TINLLDOREKRNHTL
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-538-092-1280
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   -----EPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQENPEMEGPERDQLVIP 325
                                                                                                                     DGQEEEQEAAGEGRNQ-----QKLRGEDDYNMDENEAESETDKQAALAGNDRNIDVFNVE 380
                                                                                                                                                         49 EGRVRRAAAERGAVELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNN 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chung, Soo-11
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1898;
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STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                       CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US/08/800.64*
CLASCTOTTON TO THE CONTROL OF TH
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REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 760-0404
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/056,200 FILING DATE: 30-APR-1993 ATTORNEY/AGENT INFORMATION: NAME: Pedrick, Michael F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 94, Application US/08800644
Patent No. 5958752
                                                                                                                                                                                                                                    DOKRD --- TINLL DOREKRNHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Steinert, Peter M. APPLICANT: Lee, Seung-Chul APPLICANT: Kim, In-Gyu
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SEQUENCE CHARACTERISTICS:
LENGTH: 1898 amit
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CORRESPONDENCE ADDRESS:
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US-08-800-644-94
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1208 TKRVKANLEKAKOTLENERGELANEVKVLLOGKGDSEHKRKKVEAQLOEL---OVKFNEG 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 NNDQRQQLQAL----SEPQPRLQAAGLPHTEVPQGK---GNVLGNSKSQ----TPAPSSE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 TPQVQAALSVSQENPEME----GPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNWD 353
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--EEEEKKGORGRORREREKELOFLEEEEQLORRERAQOLOEBEDGLOEDOER----RRO 883
                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR PILING DATE: 2000-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.9%; Score 161; DB 4; Length 199
Best Local Similarity 21.7%; Pred. No. 0.00017;
Matches 92; Conservative 75; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (0)...(0)
COTHER INFORMATION: Polypeptide Accession Number P35579
US-09-538-092-1077
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 1077
LENGTH: 1960
                                                            DOKRD---TINLLDOREKRNHTL 400
                                                                                                                                                                      Sequence 1077, Application US/09538092
Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                                                                      RESULT 11
US-09-538-092-1077
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RESULT 12 US-09-949-016-10872

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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-0-09
PRIOR PILING DATE: 2000-0-0-09
PRIOR PILING DATE: 2000-0-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1159 QELRSKREQEVNILKKTLEEBAKTHEAQIQEMRQK--HSQAVEBL------AEQLEQ 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1039 EEKQRQELEKTRRKLEGDSTDLSDQIAELQAQIAELKMQLAKKEEELQAALARVEEEAAQ 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKTLQRNYGRLQQDVLQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 FOXNQTNLE ----RKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVAS-----RDLSE 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 NNDQRQQLQAL----SEPQPRLQAAGLPHTEVPQGK---GNVLGNSKSQ----TPAPSSE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 VVLDSKROVE---KEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQ 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPQVQAALSVSQENPEME----GPERDQLVIPDGQEEGQEAAGEGRNQQKLRGEDDYNMD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DVFNVEDQKRDTINLLDQREKRN 397
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Sequence 863, Application US/09538092
Sequence 863, Application US/09538092
Sequence 863, Application US/09538092
GENERAL INFORMATION:
APPLICANT: Mansfield, Traci A.
TITLE 0F INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR RILING DATE: 1999-04-01
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Pred. No. 0.00017;
5; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 10872, Application US/09949016
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Best Local Similarity
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US-09-949-016-10872
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Fast:
SEQ ID NO 10872
LENGTH: 1960
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ORGANISM: Human
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US-09-949-016-11417
             ; OKGANISM: numa
US-09-949-016-6611
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Sequence 6611, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENEUR: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-0-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASLESQ for Windows Version 4.0

SEQ ID NO 6611

LENGTH: 916

TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 SLVK--VELDKKVQSLQDEVAFLRSNHEEEVADLLAQIQASHITVERK-DYLKTDISTAL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | : | | | | 270 KEIRSQLESHSDQNMHQAEEWFKCRYAKLTEAARQNKEAIRSAKEEIAEYRRQLQSKSIE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 AGLPHTEVP-----QGK------CNVLGN------SKSQTPAPS---- 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :: | | :: | | 390 KWALDIEIAAYRKLLEGEETRFSTFAGSITGPLYTHRPPITISSKIQKTKVEAPKLKVQH 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SEVVLDSKRQVEKEETNE-IQVVNEE-----PQRDRLPQEPGREQVVEDRPVGGRG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450 KFVEBIIEETKVEDEKSEMEEALTAITEELAASMKEEKKEAAEEKEEEPEAEEKAAK- 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 FGGAGELGQTPOVQAALSVSQENPEMEGPERDQLVIPDGQEEGQE------AAGEGRN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 LESVRGTKESLERQLSDIEERHNHDLSSYQDTIQQLENELRGTKWEMARHLREYQDLLNV 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KSPVKATAPEVKEEEGEKBEEE------GOEEEEEEDEGAKSDQAEEGGS 552
                                                                                                                                                                                                                                                                                                                                                                          ----ALSEPQPRLQA
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                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                           DB 4; Length 915;
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                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P07197
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                                                                                                                                                                                                                                                                       Query Match 7.9%; Score 160.5; DB 4; Best Local Similarity 19.1%; Pred. No. 6.2e-05; Matches 87; Conservative 75; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 QOKLRGE-DDYNMDENEAESETDKQAALAGNDRNID 375
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SSOTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 863
LENGTH: 915
                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                                       FEATURE
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GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPH: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-00-08
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASELSED for Windows Version 4.0
TANGTH. 11177
                                                                                                                                                                                                                                      45 IMELEGRVRRAAAERGAVELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQD-EKA 103
                                                                                                                                                                                                                                                                                                         104 VLVNNITTGERLIRVLQDQLKTLQRNYGRLQQDVL-QPQKNOTNLERKFSYDLSQCINQM 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SKSQTPAPS---- 238
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                                                                                                                         Gaps
7.9%; Score 160.5; DB 4; Length 916;
19.1%; Pred. No. 6.2e-05;
ative 75; Mismatches 149; Indels 145;
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104 VLVNNITTGERLIRVLODQLKTLORNYGRLOQDVL-OFOKNOTNLERKFSYDLSQCINOM 162	XEVKEQCEE	187ALSEPQPRLQA 211	AGLPHTEVPOGKGNVLGN	239SEVVLDSKRQVEKEETNE-IQVVNEEPQRDRLPQEPGREQVVEDRPVGGRG 288	FGGAGELGQTPQVQAALSVSQENPEMEGPERDQLVIPDGQEEEQEAAGEGRN ::	341 QQKLRGĖ-DDYNMDENEAESETDKQAALAGNDRNID 375 :::
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Search completed: June 7, 2005, 14:11:50 Job time: 46 secs

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Gannavaraph, Manjula

APPLICANT: Maderson, Dustin

APPLICANT: Thorsey of PROSTITIONS, KITS, AND

TITLE OF INVENTION: NETHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF PROSTATE CANCER

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

TITLE OF INVENTION: MATHORS: 60/310/982

PRIOR APPLICATION NUMBER: 60/310/982

PRIOR PRILNG DATE: 2001-09-25

PRIOR PELING DATE: 2001-09-25

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US-10-006-818A-100

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Sequence 2, Application US/10759803

Publication No. US20040265310A1

GENERAL INFORMATION:

APPLICANT: AFAR, Daniel B. H.

APPLICANT: HENGER, Rahan

APPLICANT: RAITANO, Arthur B.

APPLICANT: RAITANO, Arthur B.

APPLICANT: SAFFRAN, Douglas C.

TITLE OF INVENTION: NOVEL PROSTATE-RESTRICTED GENE EXPRESSED

TITLE OF INVENTION: IN PROSTATE CANCER

FILE REFERENCE: 129.13USU1

CURRENT APPLICATION NUMBER: US/10/759,803

CURRENT PILING DATE: 2004-01-16

PRIOR FLIJING DATE: 2000-04-12

PRIOR FLIJING DATE: 1990-04-12

PRIOR FLIJING DATE: 1990-04-12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQUENCE: APPLICATION OF THE PRIOR 
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100.0%; Pred. No. 2.9e-131;
cive 0; Mismatches 0; ]
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 400; Conservative
                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-177-293-184
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ORGANISM: Homo sapien
FEATURE:
NAME/KEY: SIGNAL
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APPLICANT: Wyer, Vouzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wersch, Sebastian
APPLICANT: Hersch, Sebastian
APPLICANT: Meyers, Rachel E.
APPLICANT: Meyers, Rachel E.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Meyers, Rachel E.
APPLICANT: Meyers, Rachel E.
APPLICANT: Maria, Aysegul
APPLICANT: Mysegul
APPLICANT: Milling, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: COMPOSITIONS, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: COMPOSITIONS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: COMPOSITIONS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: GORDOLOG-21
FRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
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                                                                                                                                                               DB 14; Length 400;
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Pred. No. 2.9e-131;
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100.0%; Pred. No. 2...
0; Mismatches
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Publication No. US20030124128A1
GENERAL INFORMATION:
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Kamatkar, Shubhangi
Mertens, Maureen
                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 400; Conservative
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APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-156
            LENGTH: 400
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R APPLICATION NUMBER: 60/098803
R FILING DATE: 1998-09-02
R APPLICATION NUMBER: 60/098821
R FILING DATE: 1998-09-02
R APPLICATION NUMBER: 60/098843
R FILING DATE: 1998-09-02
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RR FILING DATE: 1998-09-10
RR APPLICATION NUMBER: 60/100385
R FILING DATE: 1998-09-15
RR PFLING DATE: 1998-09-15
RR PFLING DATE: 1998-09-15
RR APPLICATION NUMBER: 60/100380
RR RFLING DATE: 1998-09-15
RR APPLICATION NUMBER: 60/100390
RR APPLICATION NUMBER: 60/100584
RR PILING DATE: 1998-09-15
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R FILING DATE: 1998-09-18

R APPLICATION NUMBER: 60/100849

PR FILING DATE: 1998-09-18

R APPLICATION NUMBER: 60/100919

R FILING DATE: 1998-09-17
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APPLICATION NUMBER: 60/099536
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FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099642
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APPLICATION NUMBER: 60/099754
FILING DATE: 1998-09-10
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FILING DATE: 1998-09-10
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APPLICATION NUMBER: 60/099808
FILING DATE: 1998-09-10
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FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099815
FILING DATE: 1998-09-10
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FILING DATE: 1998-09-16
APPLICATION NUMBER: 60/100661
FILING DATE: 1998-09-16
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APPLICATION NUMBER: 60/100711
FILING DATE: 1998-09-17
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FILING DATE: 1998-09-17
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APPLICATION UNMBER: 60/101014
FILING DATE: 1998-09-18
APPLICATION NUMBER: 60/101068
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APPLICATION NUMBER: 60/101279
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APPLICATION NUMBER: 60/099741
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FILING DATE: 1998-09-16
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FILING DATE: 1998-09-16
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FILING DATE: 1998-09-17
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FILING DATE: 1998-09-17
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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEAVASRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSE
                                                                                                                                      Gaps
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                                                                                  DB 16; Length 400;
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                                                                            Query Match 100.0%; Score 2029; DB 16; Best Local Similarity 100.0%; Pred. No. 2.9e-131; Matches 400; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR APPLICATION NUMBER: 60/098713
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
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Publication No. US20030073129A1
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Grimaldi, Christopher J.
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
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Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
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Smith, Victoria
; LOCATION: (1)...(29)
US-10-759-803-2
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US-09-946-374-100
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1998-09-22 NUMBER: 60/101471 1998-09-23 NUMBER: 60/101472 1998-09-23 NUMBER: 60/101474 1998-09-23 NUMBER: 60/101475 1998-09-23 NUMBER: 60/101475 1998-09-23 NUMBER: 60/101475 1998-09-23 NUMBER: 60/101477	1998-09-23 NUMBER: 60/10173 NUMBER: 60/10174 1998-09-24 NUMBER: 60/10174 1998-09-24 NUMBER: 60/10191 1998-09-24 NUMBER: 60/10191 1998-09-24 NUMBER: 60/1020 1998-09-29 NUMBER: 60/1023 1998-09-29 NUMBER: 60/10248 1998-09-29 NUMBER: 60/10248 1998-09-30 NUMBER: 60/10248 1998-09-30 NUMBER: 60/10248 1998-09-30 NUMBER: 60/10258	NUMBER: 60/10268 NUMBER: 60/10296 NUMBER: 60/10325 1998-10-06 NUMBER: 60/10331 1998-10-07 NUMBER: 60/10331 NUMBER: 60/10331 NUMBER: 60/10331 1998-10-07 NUMBER: 60/10339 NUMBER: 60/10339 NUMBER: 60/10339 NUMBER: 60/10339 1998-10-07 NUMBER: 60/10349 1998-10-07 NUMBER: 60/10349 1998-10-08 NUMBER: 60/10367 1998-10-08 NUMBER: 60/10367 NUMBER: 60/10367 NUMBER: 60/10367 NUMBER: 60/10363 NUMBER: 60/10367
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Sequence 486, Application US/10028072
Publication No US20030004311A1
GREBAL INPORMATION:
APPLICANT: Barer, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeFOOSE, Laura
APPLICANT: Penorge, Laura
APPLICANT: Gao, Wei-Giang
APPLICANT: Garieso, Mary E.
APPLICANT: Garieso, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Garney, Austin I.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Matanabe, Colin K PRIOR APPLICATION NUMBER: 60/104257
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: 60/104987
PRIOR APPLICATION NUMBER: 60/104907
PRIOR PLING DATE: 1998-10-20
PRIOR PILING DATE: 1998-10-20
PRIOR FILING DATE: 1998-10-20
PRIOR FILING DATE: 1998-10-20
PRIOR PILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR PILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/10569
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR PELING DATE: 1998-10-26
PRIOR PELING DATE: 1998-10-26
PRIOR PLING DATE: 1998-10-26 Query Match Best Local Similarity 100.0 Matches 400; Conservative RESULT 5 US-10-028-072-486 241 361 62 61 121 362 셤 a δ 셤 ò g ઠે Š g δ g ò Š

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THIS MESTERNER: 1997-10-28
CURRENT FEIGNION NUMBER: 05/06/9911
PRIOR APPLICATION NUMBER: 06/06/9911
PRIOR APPLICATION NUMBER: 06/06/9911
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 06/05/912
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-26
PRIOR PILING DATE: 1997-10-28
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R APPLICATION NUMBER: 60/065186
R FILING DATE: 1997-11-12
R APPLICATION NUMBER: 60/065846
R FILING DATE: 1997-11-17
R APPLICATION NUMBER: 60/066364
R FILING DATE: 1997-11-21
R FILING DATE: 1997-11-21
Wood, William
APPLICANT: Wood, Wi. APPLICANT: Zhang TITLE OF INVENTION:
                                                                                         FILE REFERENCE:
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DR FILING DATE: 1997-11-24

DR APPLICATION NUMBER: 60/066511

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DR FILING DATE: 1997-11-24

DR APPLICATION NUMBER: 60/069212

DR APPLICATION NUMBER: 60/069218

DR APPLICATION NUMBER: 60/069318

DR FILING DATE: 1997-12-11

DR APPLICATION NUMBER: 60/069314

DR FILING DATE: 1997-12-11

DR APPLICATION NUMBER: 60/069918

DR FILING DATE: 1997-12-11

DR APPLICATION NUMBER: 60/06994

DR FILING DATE: 1997-12-16 R APPLICATION NUMBER: 60/072320
RR FILING DATE: 1998-01-23
RR FILING DATE: 1998-02-04
RR FILING DATE: 1998-02-04
RR FILING DATE: 1998-02-09
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RR FILING DATE: 1998-02-09
RR FILING DATE: 1998-02-09
RR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13 R APPLICATION NUMBER: 60/080165 R FILING DATE: 1998-03-31 R APPLICATION NUMBER: 60/081203 R APPLICATION NUMBER: 60/081229 R APPLICATION NUMBER: 60/081229 R FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/079663 FILING DATE: 1998-02-27 APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27 FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081695 FILING DATE: 1998-04-15 APPLICATION UNDHER: 60/082999 FILING DATE: 1998-04-24 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083545 FILING DATE: 1998-04-29 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085579 FILING DATE: 1998-05-15 FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/086414
FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/086430
FILING DATE: 1998-05-22 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081818 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-07 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084627 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085149 APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/081817 APPLICATION NUMBER: 60/084637 APPLICATION NUMBER: 60/085697 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085704 FILING DATE: 1998-04-14 1998-05-07 ILING DATE: PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R.LGS.
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG
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Publication No. US20030022239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                          Gao, Wei-Qiang
Garritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Publication No. US20030017563A1
                                              APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Psilvaroff, Ellen
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Wood, William
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; ORGANISM: Homo Sapien
US-10-140-808-486
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Best Local S
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100.0%; Pred. No. 2.9e-131;
Live 0; Mismatches 0;
                     R FILING DATE: 1998-05-28

R FILING DATE: 1998-05-28

R APPLICATION NUMBER: 60/088026

R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-10

R FILING DATE: 1998-06-10

R APLICATION NUMBER: 60/08810

R APLICATION NUMBER: 60/08888

R APLICATION NUMBER: 60/08888

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/08959

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08959

R APLICATION NUMBER: 60/08959

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089947

R FILING DATE: 1998-06-19

R APPLICATION NUMBER: 60/090349

R FILING DATE: 1998-06-29

R APPLICATION NUMBER: 60/090429

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R APPLICATION NUMBER: 60/0904558

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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
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APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
  APPLICATION NUMBER: 60/087106
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Matches 400;
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US-10-140-808-486 ; Sequence 486, Application US/10140808

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                                                                                APPLICANT: SHELK COLOUND A
APPLICANT: Stewart. Timothy A.
APPLICANT: Stewart. Timothy A.
APPLICANT: Twansbe. Colin K
APPLICANT: Watanabe. Colin K
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: SAND, Zemin K
APPLICANT: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERRACE: P33.0RTGS4
CURRENT FILING DATE: 2002-04-16
PTIOR APPLICATION NUMBER: US/10/123,904
PTIOR APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 2029; DB 14; 100.0%; Pred. No. 2.9e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baker, Kevin P.
APPLICANT: Bereeini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith, Victoria
Stewart, Timothy A.
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Best Local Similarity 100.
Matches 400; Conservative
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APPLICANT: GOGGAGE, PAULT J.
APPLICANT: GUTNEY, AUSTIN L.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: ADANG, Semin
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APPLICANT: AD
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100.0%; Pred. No. 2.9e-131;
ive 0; Mismatches 0;
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Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Barest Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Luc
APPLICANT: Pilvaroff, Ellen
APPLICANT: Gervinen, Mary E.
APPLICANT: Gervinen, Mary E.
APPLICANT: George, Mary E.
APPLICANT: Goddard, Audrey
                                                                                       Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Matches 400; Conservative
                                                            Gao, Wei-Qiang
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ORGANISM: Homo Sapien
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US-10-123-904-486
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             APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OP INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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                                                                                                                                       Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550 SEQ ID NO 486
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Pred. No. 2.9e-131;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                           CURRENT APPLICATION NUMBER: US/10/140,470 CURRENT FILING DATE: 2002-05-06
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stewart, Timothy A
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Godowski, Paul J.
Gurney, Austin L.
Tumas, Daniel
Watanabe, Colin K
Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Watanabe, Colin K
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Matches 400; Conservative
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CORGANISM: Homo Sapien
US-10-140-470-486
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US-10-175-746-486
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100.0%; Pred. No. 2.9e-131;
iive 0; Mismatches 0;
                 FILE REFERENCE: P3330RIC353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper of the Number OF SEQ ID NOS: 550
ACIDS ENCODING THE SAME
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Publication No. US20030027275A1
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Stewart, Timothy A.
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Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
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Wood, William
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
Gao, Wei-Qiang
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Best Local Similarity 100.
Matches 400; Conservative
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ORGANISM: Homo Sapien
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US-10-176-918-486
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US-10-176-921-486
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APPLICANT: Wood, William
APPLICANT: ZENGY, EAGNIN
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RLC288
CURRENT APPLICATION NUMBER: US10/176,921
CURRENT FILING DATE: 2002-06-20
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                                                                                                   100.0%; Score 2029; DB 14;
100.0%; Pred. No. 2.9e-131;
iive 0; Mismatches 0;
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Publication No. US20030027276A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
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Wood, William
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Gurney, Austin L.
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Smith, Victoria
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Best Local Similarity 100.
Matches 400; Conservative
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                                          ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-486
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ORGANISM: Homo Sapien
NUMBER OF SEQ ID NOS:
SEQ ID NO 486
LENGTH: 401
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LENGTH: 401
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APPLICANT: Wateney, coin K
APPLICANT: Wood, william
APPLICANT: Zhang, Zemin
APPLICANTON: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C154
CURRENT APPLICATION NUMBER: US/10/137, 865
CURRENT APPLICATION NUMBER: US/202-05-03
Prior Application removed - See Palm or File Wrapper
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                Length 401;
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                      DB 14;
                   Score 2029; DB 14;
Pred. No. 2.9e-131;
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100.0%; Pred. No. 2...
0; Mismatches
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Publication No. US20030032155A1
GENERAL INFORMATION:
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
                   Query Match 100.
Best Local Similarity 100.
Matches 400; Conservative
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US-10-137-865-486
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61 AVELKKNEPOGELEKOREOLDKIOSSHNFOLESVNKLYODEKAVLVNNITTGERLIRVLO 120
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APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENE APPLICATION NUMBER: US/10/142,431
CURRENT APPLICATION DATE: 2002-05-10
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                    242 VVLDSKRQVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQ
AVELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQ
                                                                     DOLKTLORNYGRLOQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKG
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100.0%; Pred. No. 2.9e-131;
ative 0; Mismatches 0;
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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Matches 400; Conserv
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ORGANISM: Homo
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US-10-142-431-486
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APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R.C162
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 486
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                                         2 MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG
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                    MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG
                                                                                          AVELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQ
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Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 100.0
Matches 400; Conservative
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ORGANISM: Homo Sapien
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US-10-140-474-486
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US-10-759-803-2 2029 1 MGLGNGRRSMKSPPLVLAAL......DQKRDTINLLDQREKRNHTL 400 Perfect score: Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692 seqs, 386760381 residues

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seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:*geneseqp2003bs:*geneseqp2004s:* A_Geneseq_16Dec04:* geneseqp1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aab24352 Human pro	Abr47475 Breast ca	Adb75332 Prostate	Aay99368 Human PRO	Aab66117 Protein o	Aau12414 Human PRO	Aab49770 Amyloid-b	Aab93295 Human pro	Aab88480 Human mem	Abp65020 Human pro	Abo17858 Novel hum	Abu81112 Human PRO	Abu66812 Human PRO	Abu59893 Novel sec	Abo25083 Human sec	Abu67088 Human sec	Ada46005 Novel hum	Ada76436 Human PRO	Ada19086 Human PRO	Ada61709 Homo sapi			Ada86514 Novel hum	Adb16078 Human PRO	Ada47864 Human PRO
SOUTHERIES	ID	AAB24352	ABR47475	ADB75332	AAY99368	AAB66117	AAU12414	AAB49770	AAB93295	AAB88480	ABP65020	ABO17858	ABU81112	ABU66812	ABU59893	AB025083	ABU67088	ADA46005	ADA76436	ADA19086	ADA61709	ADB19494	ADB28035	ADA86514	ADB16078	ADA47864
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æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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ABO33610 ADA67659 ADB30666 ADA85962	ADA97174 ADA79478 ADA87617	ADB16819 ADA91911 ADB14974	ADB18935 ADA94150 ADB20046	ADB13358 ABO43391 ADA74612	ADB24845 ADA82369 ADA75332 ADA85410
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26 27 28 29	330	3 3 3 5 4 5	36 38 38	39 4 4 11	4 4 4 4 2 6 4 7

ALIGNMENTS

Human, prostate specific gene, 30P3C8, prostate cancer, diagnosis, cytostatic, gene therapy, vaccine, tumour. Human prostate specific 30P3C8 protein sequence SEQ ID NO:2. AAB24352 standard; protein; 400 AA 12-APR-2000; 2000WO-US010218. (first entry) WO200061610-A2. Homo sapiens. 14-FEB-2001 19-OCT-2000. AAB24352; AAB24352

99US-0128860P. (UROG-) UROGENESYS INC. 12-APR-1999;

Saffran DC; Raitano AB, Leong K, Afar DE, Hubert RS, WPI; 2000-619224/59.

N-PSDB; AAC64559

30P3C8 polypeptide and polynucleotide used for diagnosing, treating and monitoring development of prostate cancer.

Claim 1; Page 94-95; 99pp; English.

The present sequence is the human prostate specific protein 30P3CB, which is over-expressed in prostate cancer cells. 30P3CB has cytostatic activity and can be used in vaccines and gene therapy. Methods for detecting the levels of 30P3CB protein or mRNA in prostate tissue, bone tissue, lymphatic tissue, serum, blood or semen are used for diagnosing the presence of cancer in an individual or disregulated cell growth e.g. hyperplasia. The cancers which are detected or diagnosed are of the bladder, pancreas, colon, brain, bone, lung, kidney or prostate by using test samples of serum, blood or urine or tissues of the bladder, pancreas, colon, brain, bone, lung, kidney and prostate. 30P3CB polynucleotide sequences can be used for treating cancers expressing soly3CB, particularly prostate cancers. Immunogenic portions of 30P3CB are used in vaccines to inhibit the development of cancer. Anti-30P3CB

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30P2C8 and other proteins e.g. receptors for which 30P3C8 is a ligand. 30P3C8 and other proteins e.g. receptors for which 30P3C8 is a ligand. 30P3C8 may be a growth factor or other molecule involved in tumour growth and metastasis and so anti-30P3C8 antibodies may disrupt the homing or invasion or other cancer promoting activities of 30P3C8. The assays are used for detecting, staging and monitoring prostate cancer. The 30P3C8 protein or mRNA are used as additional specific markers for detecting prostate cancer and provide a more specific assay than the serum prostate specific antigen (PSA) assay
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ive 0; Mismatches 0;
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27-JUN-2001; 2001US-0301572P.
18-JUL-2001; 2001US-0306501P.
25-SEP-2001; 2001US-0352502P.
05-WAR-2002; 2002US-0362585P.
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The present invention describes a method for assessing whether a patient is afflicted with breast cancer. The method comprises comparing the level of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and ABR47386 to ABR47632) in a patient sample and the normal level of expression of the marker in a control non-breast cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with breast cancer. The breast cancer associated sequences from the present invention have cytostatic activities and can be used in gene therapy. The method is useful for diagnosing and treating breast cancer. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
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                            Myer V, Wang Y, Xu Y, Zhao X, Meyer
Pusztai L, Meric F, Sahin A, Mills
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Monahan JE, N
Hortobagyi GN,
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Prostate; cancer; cytostatic; gene therapy; marker.
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100.0%; Pred. No. 5.8e-140.
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                        25-JUL-2001; 2001US-0307982P.
22-AUG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0325020P.
                                                                                                                                                                                                                                                                                                                                                             12-DEC-2001; 2001US-0341746P. 05-MAR-2002; 2002US-0362158P.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC.
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nes 400; Conservative
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Hoersh S, Kamatkar S,
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                                                                                                           WO2003009814-A2
                                                    Homo sapiens
                                                                                                                                                                06-FEB-2003
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Human, PRO polypeptide, membrane bound protein, receptor, diagnosis, transmembrane, secretion; immunoadhesion; pharmaceutical; screening.
                                                                                                                                                                             Human PRO1326 (UNQ686) amino acid sequence SEQ ID NO:100.
361 TDKQAALAGNDRNIDVFNVEDQKRDTINLLDQREKRNHTL 400
                                                                                     AAY99368 standard; protein; 401 AA
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9805-0098821P
9805-00995843P
9805-0099598P
9805-0099602P
9805-0099642P
9805-0099642P
9805-0099741P
9805-0099763P
9805-0099808P
9805-0099812P
9805-0099815P
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980S-0100584P.
980S-0100627P.
980S-0100662P.
980S-0100662P.
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980S-0100710P-
980S-0100910P-
980S-0100849P-
980S-0100848P-
980S-0101044P-
980S-010104P-
980S-010104P-
980S-010104P-
980S-0101071P-
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98US-0101474P.
98US-0101475P.
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98US-0101479P
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RR 24-SER-1998 9 98US-0101741P
RR 24-SER-1998 9 98US-0101741P
RR 24-SER-1998 9 98US-0101741P
RR 24-SER-1998 9 98US-0101741P
RR 25-SER-1998 9 98US-0101741P
RR 25-SER-1998 9 98US-0102307P
RR 30-SER-1998 9 98US-0102307P
RR 01-OCT-1998 9 98US-0102307P
RR 01-OCT-1998 9 98US-0103348P
RR 01-OCT-1998 9 98US-0103328P
RR 01-OCT-1998 9 98US-0106328P
RR 01-NOV-1998 9 98US-0106328P
RR 01-NOV-1998 9 98US-0106332P
RR 17-NOV-1998 9 98US-0106348P
RR 18-NOV-1998 9 98US-0106348P
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AVELKKNEFOGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 VVI.DSKRQVEKEETINEIQVVNBEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQ 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention
                                                                                                                                                            New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQLKTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEBVTKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG
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                                                                                       Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 2029; DB 3; Length 401; 100.0%; Pred. No. 5.8e-140; ive 0; Mismatches 0; Indels 0
                                                                                       Watanabe CK,
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                                                                                       Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted; transmembrane; gene therapy.
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                                                                                        Gurney AL,
                                                                                                                                                                                                                       Claim 12; Fig 58; 773pp; English.
98US-0108852P.
98US-0108858P.
98US-0108904P.
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Matches 400; Conservative
                                                            (GETH ) GENENTECH INC
                                                                                        Goddard A,
                                                                                                                   WPI; 2000-237871/20.
                                                                                                                                    N-PSDB; AAA37050
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    18-NOV-1998;
                18-NOV-1998;
18-NOV-1998;
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                                                                                        Baker K,
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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TDKQAALAGNDRNI DVFNVEDQKRDTINLLDQREKRNHTL
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2000WO-US004914.
2000WO-US005004.
2000WO-US005601.
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2000US-0187202P.
2000WO-US006319.
2000WO-US006884.
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2000WO-US007532.
2000WO-US008439.
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2000WO-US014042.
2000WO-US014941.
2000WO-US015264.
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99WO-US0309911.
99WO-US030999.
99WO-US031243.
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2000WO-US003565
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2000WO-US004342
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                                                                                                                      (first entry)
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                                                                                                                                                                                                                                           WO200140466-A2
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18-FEB-2000;
18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
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03-MAR-2000;
10-MAR-2000;
15-MAR-2000;
21-MAR-2000;
30-MAR-2000;
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05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
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22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
                                                                                                                      24-OCT-2001
                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                    01-DEC-2000;
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20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
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                                                                                                AAU12414;
   361
                      362
                                                                 AAU12414
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                                                                                                                                                                                                                                                                                                                    and nucleic acids designated PRO, chromosome and gene mapping and gene
                                                                                                                                                                                                                                          Fong S;
Hillan KJ;
Watanabe C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVELKKNEFQGELEKQREQLDKI QSSHNFQLESVNKLYQDEKAVLVNNI TTGERLIRVLQ
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                                                                                                                                                                                                                                         Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                  Secreted and transmembrane proteins useful as hybridization probes, in o
                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 58; 787pp; English
                                                                                             99US-0141037P.
99US-0144758P.
99US-0145698P.
99WO-USO20111.
99US-0162506P.
99WO-USO28313.
                                                                                                                                                                        16-DEC-1999; 99WO-US030095.
05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000376.
                                                                          2000WO-US004342
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Matches 400; Conservative
                                                                                                                                                                                                                   GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                              WPI; 2001-071395/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 401 AA;
                               WO200078961-A1.
                                                                                                       20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
           Unidentified.
                                                                          18-FEB-2000;
                                                     28-DEC-2000
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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                     AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO colypeptides, to modulate biological activities of cells expressing PRO colypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO colypeptide expression in a cell sample to that in a control sample. Some colypeptide expression in a cell sample to that in a control sample. Some colypeptide expression in a cell sample to that in a control sample. Some colypeptide expression of chondrocytes, the proliferation or gene expression in periotte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-colliferation of inner ear utricular supporting cells or of T-colliferation of endothelial cells. Some of the PRO colliferation of endothelial cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polypeptides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy
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                                                                                  Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
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100.0%; Pred. No. 5.8e-140;
ive 0; Mismatches 0;
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                                                                                                                                                                                                       Claim 12; Fig 486; 813pp; English
                                                                                                                                                              cervical
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Matches 400; Conservative
                  WPI; 2001-408281/43.
N-PSDB; AAS21486.
                                                                                                                                                              breast, prostate,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide encoding Amyloid-beta protein agglutination-controlling factor, useful for inhibiting or promoting agglutination or sedimentation of amyloid-beta protein and in diagnosis and screening drugs for Alzheimer's disease.
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  Amyloid-beta protein agglutination regulating factor SEQ ID
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                                           amyloid-beta protein; agglutination regulatory
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Pred. No. 5.8e-140;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          Kawai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 56-58; 72pp; Japanese.
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100.0%; Pre
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H, Morita M;
                                                                                                                                                                                                                              06-JUL-2000; 2000WO-JP004515.
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Best Local Similarity 100.
Matches 400; Conservative
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N-PSDB; AAF29360.
                                                                Alzheimer's disease
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                                                                                                                                                WO200104299-A1
                                                                                                         Homo sapiens
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                                                                                                                                                                                         18-JAN-2001
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AAB49770 standard; protein; 401

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AAB49770

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The present interaction describes primer sets to synthemers.

[angth cDNAs defined in the specification. Where a primer set comprises:

[a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides, or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide comprises a 3'-end sequence of an oligonucleotide comprises a 3'-end sequence of combination of the polynucleotide comprises a 1'-end sequence, where the polynucleotide comprises a 1'-end sequence, where the combination of the primer sets can be used in antisense therapy and in specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in geneticitically full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and sequences; AAH3362s and AAH3333 to AAH1872 represent human coid sequences; and AAH3362s to AAH3362s copresent human amino acid sequences; and AAH3362s to AAH3362s colisons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                          Human protein sequence SEQ ID NO:12357.
                                 AAB93295 standard; protein; 401 AA.
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Sugiyama T, Wakamatsu
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11-JAN-2000; 2000JP-00118776.
02-MAX-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-002418997.
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                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                  EP1074617-A2
                                                                                                                                                                                                                                            Homo sapiens
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RESULT 8
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ö Gaps .; 0 DB 4; Length 401; Indels 100.0%; Score 2029; DB 4; 100.0%; Pred. No. 5.8e-140; ive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 400; Conservative

1 MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG

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AVELKRONEFGGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQ 121
                                                   DQLKTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKG 180
                                                                 DQLKTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKG 181
                                                                                                      NEAVASRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSE 240
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                                                                                                                                                        VVLDSKRQVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
                                                                                                                                                                      VQAALSVSQENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESE 360
                                                                                                                                                                                                                           302 VQAALSVSQENPEMEGPERDQLVIPDGQEEQQEAAGEGRNQQKLRGEDDYNMDENEAESE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secretory proteins/membrane proteins, useful in
 AVELKKNEFQGELEKQREQLDKI QSSHNFQLESVNKLYQDEKAVLVNNI TTGERLIRVLQ
                                                                                                                      182 NEAVASRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy or as candidate target molecules in drug development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 328; 609pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                              400
                                                                                                                                                                                                                                                                            362 TDKQAALAGNDRNIDVFNVEDQKRDTINLLDQREKRNHTL 401
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01-AUG-2002

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with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies andajonists of expression and activity. The antibodies and antagonists and ansays to identify modulators (agonists and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes
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Sequence 401 AA;

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                                                                                                          2 MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMBLEGRVRRAAAERG
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100.0%; Score 2029; DB 4;
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ive 0; Mismatches 0;
                                  Matches 400; Conservative
Query Match
Best Local Similarity
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ABP65020 standard; protein; 401 AA (first entry) Human protein SEQ ID 680. 25-FEB-2003 **ABP65020**

Human; expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious given disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; bacterial infection; allergy; cancer; antial-lergic; antiinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide; immunostimulant; cerebroprotective. sapiens Ношо

WO200259260-A2

The present invention relates to novel human coding sequences (ABQ99268-ABQ9608) and proteins (ABP64682-ABP65022). The sequences are useful in therapeutic, diagnostic and research methods. The polymucleotides may be used in the field of molecular biology as hybridisation probes, primers for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The collaboration for an expand of the protein of anti-sense DNA or RNA. The collaboration in diagnostics as expressed sequence tags (ESTS) for identifying expressed genes or for physical mapping of the human genome. The proteins may be used as molecular weight markers, or as nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or pluripotential state useful for re-engineering damaged or diseased tissues, transplantation, and expand cell population in a totipotential or pluripotential state useful for re-engineering damaged or diseased tissues, transplantation, and instructure of bio-pharmaceuticals or the development of bio-sensors. The polymucleotides and proteins are useful for preventing, treating or ameliorating disorders involving aberrant protein expression or colloquical activity, e.g. haemacopoietic disorders, central, peripheral nervous system diseases, mechanical and traumatic disorders, allergic varial or fungal infection, autoimmume disorders, allergic reactions and conditions, coagulation disorders, or cancer. The polymucleotide sequences of the invention were assembled from ESTS isolated mainly by sequencing by hybridisation, and in some cases, caused cancer this patent did not form part of the printed specification, but ever a sequence data for this patent did not form part of the printed specification, but ever a sequence data for this patent did not form part of the printed sequence. 62 AVELKKRIEPQGELEKQREQLDKI QSSHNFQLESVNKLYQDEKAVLVNNI TTGERLIRVLQ 121 DQLKTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKBVKEQCEERIEEVTKKG 180 AVELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQ 120 61 MGLGNGRRSWKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG NEAVASRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSE VVLDSKRQVEKEETNEI QVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQ Zhao QA; 1 MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG Gaps New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity. .<u>;</u> 100.0%; Score 2029; DB 5; Length 401; 100.0%; Pred. No. 5.8e-140; ive 0; Mismatches 0; Indels 0 Zhang J, iu C, Zhou P, Asundi V, Wehrman T, Drmanac RT; ftp.wipo.int/pub/published_pct_sequences Claim 20; SEQ ID NO 680; 394pp; English 16-NOV-2001; 2001WO-US042950. 17-NOV-2000; 2000US-00714936 Liu Tang YT, Goodrich RW, L Ren F, Xue AJ, Yang Y, Matches 400; Conservative 2002-590824/63. Local Similarity (HYSE-) HYSEQ INC N-PSDB; ABQ99606 Sequence 401 AA; 0 61 122 181 182 241 242 121 Query Match ઠે a ò qq ò d à 용 à g

2000WO-US004914. 2000WO-US005004. 2000WO-US005601.

2000WO-US004342 2000WO-US004414

2000WO-US007377. 2000WO-US007532. 2000WO-US008439.

2000WO-US030952. 2000WO-US030873. 2000WO-US032678.

2000US-00747259

2000WO-US020710 2000WO-US022031 2000WO-US023522 2000WO-US023328

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99WO-US030999
99WO-US030720
99WO-US031243
99WO-US031274
2000WO-US000219
2000WO-US000277
2000WO-US000376
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2000WO-US005841.
2000WO-US006319.
2000WO-US006884.
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2000WO-US014042.
2000WO-US014941.
2000WO-US015264.
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06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
22-FEB-2000;
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21-MAR-2000;
17-MAY-2000;
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22-MAY-2000;
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24-JUL-2000;
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24-AUG-2000;
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01-DNO-2000;
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01-MAR-2000;
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02-MAR-2000;
10-MAR-2000;
15-MAR-2000;
 antiarteriosolerotic; cardiant; anfi-infertility; anti-HTV; cytostatic; antidabetic; gene therapy; tumour necrosis factor (TNF)-alpha release; TNF-alpha release; cell proliferation; cell differentiation; gene expression modulator; proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; ALDS; acquired immunodeficiency syndrome; cancer; diabetic complication; chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing.
                                                                                                                                                          Human; secreted and transmembrane protein; PRO; antiinflammatory;
                                                                                                                                         Novel human secreted and transmembrane protein PR01326
                                TDKQAALAGNDRNIDVFNVEDQKRDTINLLDQREKRNHTL 400
                                                                                        AB017858 standard; protein; 401 AA
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98WO-US019330.
98WO-US019437.
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98WO-US022992.
98WO-US024855.
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99WO-US005028.
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99WO-US021090,
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20-APR-1999;
14-MAY-1999;
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01-SEP-1999;
08-SEP-1999;
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10-SEP-1998;
14-SEP-1998;
14-SEP-1998;
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16-SEP-1998;
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29-OCT-1998;
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Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G. Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; 2001US-00860216. 2001US-00866028. 2001US-00866034. 2001US-00872035. 2001WO-US017800. 2001US-00874503. 2001WO-US006666. 2001US-00802706. 2001US-00808689. 2001US-00816744. 2001US-00828366. 2001US-00854208. 2001US-00854280. 2001US-00882636. 2001US-00886342. 2001WO-US019692. 2001WO-US020116 2001WO-US021066 09-AUG-2001; 2001US-00927796 16-AUG-2001; 2001US-00931836 19-DEC-2001; 2001US-00028072 2001US-00796498 2001WO-US006520 2001WO-US017092 2001US-00887879 (GETH) GENENTECH INC WPI; 2003-341980/32. N-PSDB; ACD24095. 01-MAR-2001; 09-MAR-2001; 22-MAR-2001; 22-MAR-2001; 05-APR-2001; 10-MAY-2001; 10-MAY-2001; 01-JUN-2001; 2 01-JUN-2001; 2 05-JUN-2001; 2 19-JUN-2001; 2 20-JUN-2001; 2 21-JUN-2001; 2 22-JUN-2001; 2 29-JUN-2001; 2 25-MAY-2001; 25-MAY-2001; 18-MAY-2001; 25-MAY-2001; 14-JUN-2001;

Gao W;

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has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nuclectide sequences, and which encodes a corresponding of 275 nuclectide sequences, and which encodes a corresponding colypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a comparation of properties activity of a cell, stimulate the release of tumour necrosis factor (TKP) alpha from human blood, modulate the uptake of glucose or free fatty acid by cells, stimulate the crimilate the telease of proteoglycans, stimulate the release of cytokine from peripheral blood mononuclear cells, inhibit the binding of A-peptide from peripheral blood mononuclear cells, inhibit the binding of A-peptide coded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and this is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                          The invention describes an isolated nucleic acid (I) comprising, or which
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                                                inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency
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                          secreted and transmembrane PRO nucleic acids, for treating
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                                                                                                                                                       Claim 12; Fig 486; 660pp; English.
                                                                                                 syndrome (AIDS), or cancer
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Human PRO polypeptide #243.
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anti-PRO antibody, diagnostic assay, gene expression, diabetes, bone disorder, cartilage disorder, rheumatoid arthritis, obesity, sports injury, osteoarthritis, hyper-insulinaemia, hypo-insulinaemia, hearing loss, coagulation disorder, stroke, heart attack, cardiant, antidiabetic, anorectic, vulnerary, antiarthritic, osteopathic, antirheumatic, auditory, cerebroprotective, angiogenic. polypeptide; secreted and transmembrane protein;

Homo sapiens.

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US2003004311-A1.
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02-JAN-2003

19-DEC-2001;

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97US-0049911P.
97US-0056974P.
97US-0059113P.
97US-0059115P.
97US-0059117P.
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17-SEP-1997

970S-0059184P. 970S-0059263P. 970S-005932P. 970S-0059836P. 970S-0062250P. 970S-0062285P. 970S-0062287P. 19-SEP-1997 17-0CT-1997

24-0CT-1997; 24-0CT-1997; 24-0CT-1997; 24-0CT-1997; 24-0CT-1997;

27-OCT-1997

27-OCT-1997; 28-OCT-1997; 28-OCT-1997;

9705-0062814P 9705-0062816P 9705-00633042P 9705-0063329P 9705-0063329P 9705-006350P 9705-006350P 9705-006373P 9705-006373P 9705-006373P 9705-006373P 9705-006373P 9705-006373P 9705-006373P 9705-006373P 9705-006424P 9705-006424P 9705-006651P 9705-006651P 9705-006651P 9705-006651P 29-OCT-1997

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97US-0069334P. 97US-0069694P. 98US-0072320P. 98US-0073612P 04-FEB-1998; 16-DEC-1997 11-DEC-1997 11-DEC-1997

98US-0074086P. 98US-0074092P. 98US-0077791P. 98US-0078910P.

98US-0079663P 98WO-US014552 98US-00797

28-AUG-1998; 10-SEP-1998;

98WO-US017888. 98WO-US018824. 98US-0080165P

23-JUN-2003 (first entry)

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61 AVELKKNEFØGELEKØREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQ 120
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polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at segdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                      2 MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG
                                                                                                                                                                                                                                                                         DOLKTLORNYGRLOODVLOFOKNOTNLERKFSYDLSOCINOMKEVKEOCEERIBEVTKKG
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tumour necrosis factor-alpha; TNF-alpha; blood, proliferation,
differentiation, chondrocyte; tumour, genetic disorder; cytostatic.
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                                                                                                        Length 401;
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                                                                                                        Query Match 100.0%; Score 2029; DB 6; Best Local Similarity 100.0%; Pred. No. 5.8e-140; Matches 400; Conservative 0; Mismatches 0;
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98WO-US022991
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17-SEP-1998;
07-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated PRO polypeptide useful for treating diabetes, rheumatoid arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or heart attack.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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98WO-US024855.
98WO-US025108.
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11-FEB-2000; 2
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99WO-US005028.
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25-MAY-2001; 2001WO-US017092.
01-JUN-2001; 2001US-00872035.
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09-MAR-2001;
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24-AUG-2000;
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New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                20-JUN-2001; 2001WO-US019692.
22-JUN-2001; 2001US-0088779.
22-JUN-2001; 2001WO-US021016.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US0827066.
18-JUL-2001; 2001WS-0098827.
06-AUG-2001; 2001US-00924419.
19-AUG-2001; 2001US-00927796.
16-DEC-2001; 2001US-009287796.
        2001US-00874503.
2001US-00882636.
2001US-00886342.
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N-PSDB; ACA03845.
        05-JUN-2001; 14-JUN-2001; 19-JUN-2001;
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Sequence 401 AA;

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DQLKTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKG 180
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100.0%; Score 2029; DB 6; Length 401; 100.0%; Pred. No. 5.8e-140; Live 0; Mismatches 0; Indels 0;
                         Best Local Similarity Matches 400; Conservative
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VQAALSVSQENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESE 360
242 VVLDSKRQVEKEETNBIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQ 301
                                                                                                                                                                   Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
                       361 TDKQAALAGNDRNIDVFNVEDQKRDTINLLDQREKRNHTL 400
                                                       TDKQAALAGNDRNIDVFNVEDQKRDTINLLDQREKRNHTL 401
                                                                                                                                                     Novel secreted and transmembrane protein PR01326
                                                                                                     ABU59893 standard; protein; 401 AA
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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ME, Goddard P
Stewart TA, T
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Gerritsen N
Smith V,
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2003-148238/14.

ABO25083 standard; protein; 401 AA.

05-SEP-2003 (first entry)

AB025083;

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The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in conduction a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO colypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO5186, PRO943, PRO828, PRO826, PRO943, PRO828, PRO826, PRO943, PRO944,                                                                                     Two hundred and seventy five nucleic acids encoding PRO polypeptides, useful for treating pericyte-associated tumors, diabetes and various bone and/or cartilage disorders, e.g. arthritis.
                                                                                                                                                                                                                  Claim 12; Fig 486; 659pp; English
                             N-PSDB; ABX89383
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Length 401; Indels 100.0%; Score 2029; DB 6; 100.0%; Pred. No. 5.8e-140; ive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 400; Conservative Sequence 401 AA;

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Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic; gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood; proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell; PBMC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell; chondrocyte cell proliferation; chondrocyte cell proliferation; chondrocyte cell differentiation; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell; A-peptide; factor VIIA.
                                               Human secreted/transmembrane protein (PRO) #243.
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(GETH) GENENTECH INC.

3 Gao L, Filvaroff E, (y AL, Sherwood S; Wood WI, Zhang Z, Deforge L, Desnoyers L, A, Godowski PJ, Gurney AL Tumas D, Watanabe CK, Woc Baker KP, Beresini M, De Gerritsen ME, Goddard A, ME, GODDARG Stewart TA, Gerritsen ME, Smith V,

2003-466355/44. N-PSDB; ACD42037. WPI;

isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 1978, useful in molecular biology, chromosome and gene mapping, PRO4978, useful in molecular biology, chromosome and g generating antisense RNA and DNA, and in gene therapy. New

or in

Claim 12; Fig 486; 659pp; English.

80% The invention relates to an isolated nucleic acid comprising at least sequence identity to a PRO (secreted and transmembrane protein) cDNA comprising a nucleic acid (a) encoding a PRO polypeptide, or is extracellular domain (with or without its associated signal peptide),

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which comprises any of the 275 120-850 residue amino acid sequences, cg given in the specification; (b) comprising any of the 275 300-3500 nucleotide sequences given in the specification; or (c) comprising the full-length coding sequence of the nucleotide sequence given in the specification, or of the DNA deposited under any of the American Type (c) the collection (ATCC) Accession Numbers listed in the specification. Also included are a vector comprising the novel nucleic acid, a host cell comprising the vector, producing a RPO polypeptide, the isolated RRO polypeptide of fused to a heterologous amino acid sequence, an anti-RRO polypeptide of fused to a heterologous amino acid sequence, an anti-RRO antibody, detecting a RRO polypeptide in a sample suspected of containing the RPO polypeptide, inking a bacat one bloodycal activity of a cell expressing a PRO polypeptide, simulating the release of tumour necrosis cartilage or cytokine from peripheral blood emonuclear cells (pubm()), modulating the uptake of glucces or FRA by skeletal muscle cells or factor-alpha (TMF-alpha) from human blood, (or proteoglycans from cartilage or cytokine from peripheral blood emonuclear cells (or proliferation of imner ear utricular supporting captigoryte cells, stimulating the proliferation of inner ear utricular supporting cells, stimulating the proliferation of inner ear utricular supporting cells, or of r-lymphocyte cells, or of endochellal or cells, in the proliferation of inner ear utricular supporting cells, or of T-lymphocyte cells, or of endochellal or cells
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OM protein - protein search, using sw model

Run on:

June 7, 2005, 13:57:30 ; Search time 170 Seconds (without alignments) 1204.892 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-759-803-2 2029 1 MGLGNGRRSMKSPPLVLAAL.....DQKRDTINLLDQREKRNHTL 400

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 Total number of hits satisfying chosen parameters: 1612378 seqs, 512079187 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q8nbj4 homo sapien	_	Q7zuc8 brachydanio	Q6p0h0 brachydanio	Q641d4 xenopus lae		_	Q6p2l7 mus musculu	Q6uy45 homo sapien	Q6rzw5 mus musculu	Q8c4z2 mus musculu	Q7t0x8 xenopus lae	Q96eml homo sapien	Q25142 halocynthia	Q75ue0 lampetra ja	Q75uel lampetra ja	_				Q7qii2 anopheles g	Q78473 neurospora	P02566 caenorhabdi	Q7pf85 anopheles g	Q9c0b4 homo sapien	Q7z2l3 homo sapien	P73340 synechocyst		Q8i2d8 plasmodium		Q26079 placopecten
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## ALIGNMENTS

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PRT; 401 AA.  puence update) notation update) membrane protein GP73) (UNQ686/PRO1 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	SEQUENCE FROM N.A., ALTERNATIVE INITIATION, GLYCOSYLATION, TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION. SPECIFICITY, AND SUBCELLULAR LOCATION. MEDISUB-20293047; Pubmed-10831838; DOI=10.1016/S0378-1119(00)0013 Kladney R.D., Bulla G.A., Guo L., Mason A.L., Tollefson A.E., Simon D.J., Koutoubi Z., Fimmel C.J.; "GP73, a novel Golgi-localized protein upregulated in viral infection.";	R., a. H., hii hii hii hii hii hii hii hii hii hi	Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase TO., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nuasashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriyama H., Satoh N., Takami S., Terashima Y., Suzuki O. Moriyama H., Satoh N., Takami S., Terashima Y., Suzuki O. Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Yamagai A., Itakura S., Fukuzumi Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S Okitani R., Kawakami T., Noguthi S., Itoh T., Shigeta K., Sana T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Makagawa K., Mizuno T., Shirai Y., Takahashi Y., Nakagawa K., Mizuni M., Salaki M., Matsuwa K., Nagase T., Namura N., Kikuchi H., Masuho Y., Yamashita R. Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
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vector (DDONR201)."
"Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                    MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Lewing A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Van G., Yau G., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=12029628; DOI=10.1053/jhep.2002.32525; Kladney R.D., Cui X., Bulla G.A., Brunt E.M., Fimmel C.J.; "Expression of GP7." a resident Golgi membrane protein, in viral and nonviral liver disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FubMed=12359426; DDI=10.1006/viro.2002.1523; Kladney R.D., Tollefson A.E., Wold W.S., Fimmel C.J.; Kladney R.D., Tollefson A.E., Wold W.S., Fimmel C.J.; Fipmed C.J.; Integralation of the Golgi protein GP73 by adenovirus infection virology 301:236-246(2002). "Fipmed C.J."; Fipmed C.J. "Fipmed C.J."; Fipmed C.J. "Fipmed C.J. "Fipm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
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Puri S., Bachert C., Fimmel C.J., Linstedt A.D.;
"Cycling of early Golgi proteins via the cell surface and endosomes
upon lumenal pH disruption.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The secreted protein discovery initiative (SPDI), a large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                         Nat. Genet. 36:40-45(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences."
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
     ALTERNATIVE PRODUCTS:

Event=Alternative initiation;

Event=Alternative initiation;

Comment=2 isoforms, 1 (shown here) and 2, are produced by alternative initiation at Met-1 and Met-11;

Comment=2 isoforms, 1 (shown here) and 2, are produced by alternative initiation at Met-1 and Met-11;

-:- TISSUE SPECIFICITY: Widely expressed. Highly expressed in colon, prostate, trachea and stomach. Expressed at lower level in testis, muscle, lymphoid tissues, white blood cells and spleen. Predominantly expressed by calls of the epithelial lineage. Expressed at low level in normal liver. Expression significantly increase in liver disease due to non-viral causes (alcohol-induced liver disease, autoimmune hepatitis). Increased expression in hepatocytes appears to be a general feature of advanced liver disease. In liver tissue from patients with adult giant-call hepatitis (GCH), it is strongly expressed in hepatocyte-derived syncitial giant calls. Constitutively expressed by biliary epithelial cells but not by hepatocytes.

-:- INDUCTION: Up-regulated in response to viral infection. Induced by the man.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AVELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQ 120
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Golgi phosphoprotein 2, isoform 2.
For isoform 2.
Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Lumenal (Potential).
Coiled coil (Potential).
N-linked (GlONAC. .) (Potential).
N-linked (GLONAC. .) (Potential).
N-linked (GLONAC. .) (Potential).
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EMBL; AK075542; BAC11685.1; -.
EMBL; AX358593; AAQ88956.1; -.
EMBL; CR457201; CAG33482.1; -.
EMBL; BC001740; AAH01740.1; -.
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STRAINE-VB/N; TISSUE-Salivary gland;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1078; Matchen N.C., Manch N.C., Manch N.C., Manch N.C., Manch N.C., Cardinic P., Frange C., Marchen M.J., McKernan K.J., Mallahy S.J., Manch S.A., McEwan P.J., McKernan K.J., Mallahy S.J., Manch S.A., McEwan P.J., McKernan K.J., Mallahy S.J., M.C., Mallah S.J., Manch M.C., Gaby M.C.,
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  241
                                                   VVLDSKRQVEKBETNEI QVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQ 300
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                                                                                     242 VVLDSKRQVEKEETINEIQVVNEEPQRDRLPQEPGREGVVEDRPVGGRGFGGAGELGQTPQ
NEAVASRDLSENNDÓRQOLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSE
                                                                                                                                                                                         PTM: Glycosylated (By similarity). CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
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-!- FUNCTION: Unknown. Cellular response protein to viral infection
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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INDUCTION: Up-regulated in response to viral infection (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 45, Created)
(Rel. 45, Last sequence update)
(Rel. 45, Last annotation update)
hoprotein 2 (Golgi membrane protein GP73).
                                                                                                                                                                                                                                                                   TDKQAALAGNDRNIDVFNVEDQKRDTINLLDQREKRNHTL 400
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MGD; MGI:1917329; Golph2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Golgi phosphoprotein 2
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Q91XA2;
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TISSUE=Monle body;

XX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XA Strausberg R.L., Feingold B.A., Grouse L.H., Derged J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Habseh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ugdin T.B., Toshlyviki S., Carninci P., Parage C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D. Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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                                                                                                                                                                                                       Gaps
Golgi stack; Signal-anchor; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                           Lumenal (Potential).
Coiled coil (Potential).
N-linked (GlCNAc. . .) (Potential).
N-linked (GlCNAc. . .) (Potential).
N-linked (GlCNAc. . .) (Potential).
B19897C9D6D3618F CRC64;
                                                                                                                                                                                                       19;
                                                                                                                                                                      DB 1; Length 393;
                                                                                                                                                                                                     68; Indels
             Cytoplasmic (Potential).
Signal-anchor for type II
protein (Potential).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein zgc:56525.
ORFNames=zgc:56525;
                                                                                                                                                                    ; Score 1196.5; DB ]
; Pred. No. 4.2e-49;
51; Mismatches 68;
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393 AA;
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DOMAIN
CARBOHYD
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TRANSMEM
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CARBOHYD
SEQUENCE
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                               60 GAVELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVL 119
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 Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EREEKSKIKAEDEMHRQNEQLELMEKTHHRQOENAINSWRQEKENLQLNISSSAKAVQNM
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Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                               20.8%; Score 4.2, 2.26.8%; Pred. No. 1.5e-12; tive 96; Mismatches 124; Indels 102;
                                                                                                                SEQUENCE FROM N.A. TISSUE-Whole body; Strausberg R.; Strausberg R.; Strausberg (WAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                             45462 MW; 0521526362E3D29B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 AA
                                                                                                                                                          EMBL; BC049324; AAH49324.1; -. ZFIN; ZDB-GENE-040426-1060; zgc:56525.
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                                                                                                                                                                                                                                        Matches 118; Conservative
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                                                                                                                                                                                   al protein.
411 AA; 4
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ORFNames=zgc:56525;
                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                  Hypothetical
SEQUENCE 41
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Straubberg R.L., Feingold E.A., Grouse J.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Rhopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Branstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Anderszion and initial analysis of more than 15,000 full-length human
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Straubberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC065624; AAH65624.1;
ZPIN; ZDB-GENE-040426-1060; zgc:56525.
SEQUENCE 410 AA; 45332 MW; DC6BCBC54515EE25 CRC64;
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25-OCT-2004 (TEMBLrel. 28,
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Matches 115; Conservative
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TISSUE=Blood;
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Klausner R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.R., Shalar N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wishin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raber J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Nones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIEEVTKKGNEAVASRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLRRASGKGGTVA----QEENADTOKTO---KPKTIL----LKDLIQKOEKQNPLQNIQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQTPAPSSEVVLDSKRQVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 VRRAAAERGAVELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 GERLIRVLQDQLKTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --PSSPV-----KEETNDKPGAIPNPD---LKQEPAKDSITDE--LANKLKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                          Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                              MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                               "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein S., Gerhard D.S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082403; AAH82403.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2403; AAH8Z403.1; -.
355 AA; 39896 MW; 654DBE8944FC6F05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
    OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.5%; Score 416.5; DB 235.5%; Pred. No. 2.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                      Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123; Conservative
                                                                                                                            Xenopodinae; Xenopus.
                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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25-OCT-2004 (TrEM)
MGC82000 protein.
Name=MGC82000;
                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSUE=Kidney;
                                                                                                                                                                                                                                                                                                                     initiative.
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TISSUE=Blood,

MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Fearbaold E.A., Grouse L.H., Derge J.G.,

Rausner R.D. (Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green R.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Gones S.J., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 K------LADOFLEEOKOETOKIOSNDGKE-----LDINNOVVPKNIPKVAENVADKN 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 EEPSSNHIPHGKEQIKRGGDAGMPGIEENDLAKVDDLPPALRKPPISVSQHESHQAISHL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VGFGANRRAGRLPSLVLVVLLVVIVVLAFNYWSISSRHVLLQEEVAELQGQVQRTEVARG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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384
                                         267 EQGPL---NDYNGDEGNEAEPEADKQAELA-DDQNVNEDNPAQEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063480; AAH63480.1; -.
340 NQQKLRGEDDYNMDE-NEAESETDKQAALAGNDRNIDVFNVEDQKR
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SEQUENCE 433 AA; 48864 MW; 3895383DC2D3F106 CRC64;
                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                  433
                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 27, (TrEMBLrel. 27, I (TrEMBLrel. 27, I
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fatches 111, Conservative
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                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                            PTGQPLSPNMPPDSHINHNGNPGTSKQNPSSPLQRLIPGSNLDSEPRIQTDILKQATKDR 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIRVLQDQLKTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KIQSNDGKELGRNDHGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------EEQEAAGEGRNQQKLRGEDDYNMDE-NEAESETDKQAALAGNDRNIDV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 NDFHKLKOSRFFDENESPVDPQHGSKLA---DYNGDDGNVGEYEADKQAELAYNEEEDGD 372
                     ---RGFGGAGELGQTPQVQAALSVSQENPEMEGPERDQLV---- 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVELKKNEFOGELEKQREOLDKIQ-----SSHNFQLESVNKLYODEKAVLVNNITTGER 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVTKKGNEAVASRDLSENNDORQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-----KNI PNVPENDANK----NEDPSSNHLPH--GKEQL---KRVGDAGMPGVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAPSSEVVLDSKROVEKEETNEIQVVNNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --LGQTPQVQAAL----SVSQENPE-----MEGP--ERDQLVIPDGQE----
                                                                                                                                            349 VSDFHKLKQSRFFDENESPVDPQHGSKLA---DYNGDDGNVGEYEADKOAELAYNE 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Craniata, Vertebrata, Buteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                       -- EEQEAAGEGRNQQKLRGEDDYNMDE-NEAESETDKQAALAGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.2%; Score 348; DB 2; Length 40
26.5%; Pred. No. 5.2e-09;
ive 76; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6J;
Zhou G., Liu X., Li H.;
Zhou G., Liu X., Li H.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY8484581; AAR56704.1; -.
SEQUENCE 402 AA; 45913 MW; 906EB9162B6A7F9A CRC64;
                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Matches 116; Conservative
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VGFG2573 isoform 1
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05-JUL-2004
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05-JUL-2004
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STRAIN=CSTRL/6; TISSUE=Brain;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Ralausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Barder T., Schaefer C.F., Bhat N.K.,

B Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

D Districtench C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahe J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Galimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AVELKKNEFQGELEKQREQLDKIQ-----SSHNFQLESVNKLYQDEKAVLVNNITTGER 114
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Sciurognathi, Muridae, Murinae, Mus.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 435 AA; 49408 MW; C62F71B6B2FA7598 CRC64;
27, Last annotation update)
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Pred. No. 7.5e-09;
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STRAIN=C57BL/6; TISSUE=Brain;
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Mammalia; Butheria;
NCBI_TaxID=10090;
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VGFG2573 iso
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
EMBL, AY38086; AAQ88453.1; --
SEQUENCE 380 AA, 43332 MM; B99B88414F734501 CRC64;
                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SPDI), a large-scale
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.0%; Score 324; DB 2; Length 38 25.1%; Pred. No. 6.7e-08; ive 71; Mismatches 175; Indels
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Last annotation update)
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                                                                                                                      (TrEMBLrel.
                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                     ORFNames=UNQ2573;
Homo sapiens (Human).
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Q6UY45;
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61 AVELKKNEFQGELEKQREQLDKIQ----SSHNFQLESVNKLYQDEKAVLVNNITTGER 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K------KIQSNDGKETH------K12SNDGKELGRNDHGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAPSSEVVLDSKRQVEKEETNEIQVVNREPQRDRLPQEPGREQVVEDRPVGGRGFGGAGE 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LGOTPQVQAALSVSQ-ENP--EMEGPERD-QLVIP----DGQEEEQEAAGEGRNQQKL 344
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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                                                                                      Craniata, Vertebrata, Buteleostomi,
Sciurognathi, Muridae, Murinae, Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MIXEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length en library, clone:A630071M09 product:hypothetical protein, full
                                                                                                                                                                                                                                                                                                                                                                                                                           15.4%; Score 312; DB 2; Length 319; 26.9%; Pred. No. 2e-07; ive 64; Mismatches 137; Indels (
                                                                                                                                                                                                                                                                    Zhou G., Liu X., Li H.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY404585; ARZ6705.1; -
SEQUENCE 319 AA, 36067 WW, D7D9308F3A2063FC CRC64;
27, Last annotation update)
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                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
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01-MAR-2003 (TrEMBLrel. 23,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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(TrEMBLrel.
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                                                         musculus (Mouse)
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Name=D130060C09Rik;
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                            isoform 2
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA sequences.";
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                                                                                                                  Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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                                          MGC68898 protein.
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

C STRAIN=C57BL/6J; TISSUE=Thymus;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci D., Fukuda S., Furuno M., Hanaqaki T., Hara A., Hashizume W., Hayatuno M., Hanaqaki T., Haraka T., Hirozane T., Hori F., Indyanida K., Ishi Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Akamura M., Nishi K., Nomura K., Numazaki R., Murata M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Toya T., Yasunishi A., Muramatsu M., Hayashizaki T., Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                         the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                            STRAIN=C57BL/6J; TISSUB=Thymus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Shibata ton and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGLGNGRRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 LIRVLQDQLKTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 DIHHLKEQLAELRQEFLRQEDQLQDYRKNNTYLVKRLEYESFQCGQQIKELRAQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%; Score 255; DB 2; Length 17
33.3%; Pred. No. 5.1e-05;
tive 39; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 AA; 20591 MW; 4C1E31550D086704 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
                       STRAIN=C57BL/6J; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK080364; BAC37891.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 33.3
nes 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                            FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
                                                                                                                                                                 SEQUENCE FROM N.A.
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Q7TOX8; 01-OCT-2003 (TrEMBLrel. 25, Created)

RESULT 12

Q7T0X8

HAU

Best Loc Matches

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Straubberg R.L., Feingold B.A., Grouse L.H., Distons. 442003899;

Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Anterchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Wilalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Schwuck Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AVELKKNEFQGELEKQREQLDKIQSSH-----NFQLESVN-KLYQDEKAVLVNNITTGER 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 LIRVLQDQLKTLQRNYGRLQQDVLQPQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 PAPSSEVVLDSKRQVEKEETNEIQVVNEEPQRDRLP------------QBPGR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TVDNKMHILPSEVKE---KIEDPSSNRLPFAQDGIKLESDAGMPEIEDNEPAK 249
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                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.9%; Score 241; DB 2; Length 356; 21.5%; Pred. No. 0.00052; ive 72; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S., Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC055994; AAH55994.1; -.
SEQUENCE 356 AA; 40767 MW; 2C868BD7FFB5FB42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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laevis (African clawed frog)
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Query Match
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Q75UE0
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Alausher R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bahat N.K.,
A popkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,
Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bromstein M.J., Usdin T.B., Ronaldo M.F., Gasavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Glubs R.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Krzyninski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
EQVVEDRPVGGRGFGGAGE----LGQTPQVQAALSVSQENPEMEGPERDQLV-IPDGQE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AVELKKNEFQGELEKOREQLDKIQ-----SSHNFQLESVNKLYQDEKAVLVNNITTGER 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                   250 EDSLQN-DVKGQDTGALPSQSKSLLEKQPSLQ-PLSFTEHEVKKPLPDKKETVOIP---E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VGFGANRRAGRLPSLVLVVVLLVVILVVILAFINYWSISSRHVLLQEEVAELQGQVQRTEVARG
                                                                                                                                                                                                                                                             Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 LIRVLODQLKTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLS--QCINQMKE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIHHLKEQLAELRQEFLRQEDQLQDYRKNNTYLVKRLEYESKRFKRFNQMME 173
                                                                           1: | : | | : | | 305 VEENALQLEPHPLKQMPRDSKTMSFNLKQKDDDHDGQADAGEYHKDHLN 353
                                                      330 BEQEAAGEGRNOOKLRGEDDYNMDENEAESETDKOAALAGNDRNIDVFN 378
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.6%; Score 235; DB 2; Length 177; 33.1%; Pred. No. 0.00045; ive 37; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012124; AAH12124.1; -.
SEQUENCE 177 AA; 20934 MW; DF8452919A90949A CRC64;
                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                         Homo sapiens (Human).

Bukaryota, Metazoa, Chordata,
Mammalia, Butheria, Primates,
MCBI_TaxID=9606;
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(TrEMBLrel. 19, L
(TrEMBLrel. 22, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 33.1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.
                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  H63 protein.
                                                                                                                                                                                    01-DEC-2001
01-DEC-2001
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Q25142
ID Q2514
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1170 EFSKLRRELEESNIAHEATVSTLRKKKHADSSAEMSEOIDNLORVKOKLEKEKSEMKMEVD 1229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1315 LKRVVE-EETKAKAALAHSVQASRHDNDLLREQYEEEQEA------KAELQRA 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKTLQRNYG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 RLQQDV------LQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 ASRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSEVVLD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 SKRQVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 LSVS-----AGEGRNQQK 343
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Araki I., Satoh N.;
"Cis-regulatory elements conserved in the proximal promoter region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1361 LSKANAEVAQWRNKYETDAIQRTEELEEAKKKLATRLQEAEEQVEATQAKCASLDKTKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail 1; 1.
PRINTS; PR0193; MYOSINHEAVY.
SMART; SM0424; MYSC; 1.
SEQUENCE 1927 AA; 222461 MW; 2F6F18A2B71BC34E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      an ascidian embryonic muscle myosin heavy chain gene.";
Roux's Arch. Dev. Biol. 0:0-0(1995).
EMBL: 945163; BRA08111.1; -.
PIR; A59236; A59236.
HSSP; P08799; IMND.
                                                                                                                                                     Bukaryota, Metazoa, Chordata, Urochordata, Ascidiacea,
Stolidobranchia, Pyuridae, Halocynthia.
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.9%; Score 200.5; DB 2; 23.1%; Pred. No. 0.29; ive 57; Mismatches 151;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 DLQTRIMELEGRVRRAAAERGAVELKKNEFQGELE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016459; C:myosin; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003774; F:motor activity; IEA.
InterPro; IPR00169; Myosin.
InterPro; IPR004609; Myosin.head.
InterPro; IPR004609; Myosin.N.
InterPro; IPR02928; Myosin.Tail.
                                                                                           Embryonic muscle myosin heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00612; IQ; 2.
Pfam; PF00063; Myosin head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 23.18
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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994 AAAALDKKQKAFDKILSEWKQKYEESQSELEASQKESRSLSTEVFKLKNAYEETLDHLET 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 SVNKLYQD-EKAVLVNNITTG-----ERLIRVLQDQLKTLQRNYGRLQQDVLQFQKNQT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              726 EFOKLRRDLEEATLOHEATAAALRKKQADSVAELGEQIDNLORVKQKLEKEKSEFKMEVD 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLERKFSYDLSQCINOMKEVKEQC---EERIEEVTKKGNEAVASRDLSENNDQRQQLQAL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-EPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSEVVLDSKRQVEKEETNEIQVVN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVS------ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 ET-----NIDVFNVEDQKRDTINLIDQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 DLQTRIMELEGRVRRAAAERGAVELKKNEFQGELEKQREQLDKIQSSHNFQLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- QENPEMEGPERDQLVIPDGQEEEQEA----AGEGRNQQKLRGE-DDYNMDENEAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                       Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lethenteron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.1%; Score 185.5; DB 2; Length 1491; 22.0%; Pred. No. 1.1; tive 81; Mismatches 154; Indels 99;
                                                                                                                            Kusakabe R., Takechi M., Tochinai S., Kuratani S.;
Kusakabe R., Takechi M., Tochinai S., Kuratani S.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126174; BaD01607.1; -.
HSSP; P24733; 1KK7.
RGO; GO:000524; F:ATP binding; IEA.
GO; GO:0003774; F:moror activity; IEA.
RGO; GO:0003774; F:moror activity; IEA.
RICEPPO; IPR001609; Myosin. head.
InterPro; IPR001609; Myosin. head.
InterPro; IPR001609; Myosin. tail.
InterPro; IPR001633; Tropomyosin.
R InterPro; IPR00153; Tropomyosin.
R Pfam; PF00163; Myosin. head; 1.
R Pfam; PF00194; TROPOMYOSIN.
R PRINTS; RR00194; TROPOMYOSIN.
R PRINTS; RR00194; TROPOMYOSIN.
R PRINTS; RR00194; MYSO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 1491 AA; 172783 MW; 1EF0875BB3E3AF37 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Myosin heavy chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 22.0
Matches 94; Conservative
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1054 LKRENKNL 1061
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rch completed: June 7, 2005, 14:07:33 time : 180 secs

Search Job tim

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                 Copyright
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- protein search, using sw model OM protein

June Run on:

7, 2005, 14:01:01; Search time 41 Seconds (without alignments) 938.700 Million cell updates/sec

US-10-759-803-2 2029

score: Title: Perfect

1 MGLGNGRRSMKSPPLVLAAL......DQKRDTINLLDQREKRNHTL 400 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

seq length: 0 seq length: 200000000 0B 0B Minimum 1 Maximum 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		df			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
	200.5	9.6	1927	7	A59236	embryonic muscle m
7	185	9.1	1974	~	T30010	hypothetical prote
e	178.5	8.8	1963	٦	MWKW	
4	176	8.7	1200	~	S77524	chromosome segreda
5	176	8.7	3498	7	T22330	hypothetical profe
9	174	9.8	1738	~	T14867	
7	172.5	8.5	1175	7	C35815	myosin heavy chain
ω	172.5	8.5	1201	~	A35815	heavy
σ	172	8.5	1175	ď	D35815	
10	172	8.5	1201	ď	B35815	myosin heavy chain
11	171.5	8.5	1164	N	T24806	hypothetical prote
12	171.5	8.5	1938	Н	A40997	>
13	170.5	8.4	1940	~	A59287	
14	170	8.4	2385	7	A32491	
15	170	8.4	2411	7	B32491	myosin heavy chain
16	169.5	8.4	1269	ď	F84730	
17	168.5	8.3	1938	7	A59293	skeletal myosin he
18	168	8.3	1922	N	T00637	hypothetical prote
19	167.5	8.3	1956	~	T16416	
20	167.5	8.3	1957	7	A45627	myosin heavy chain
21	167	8.2	849	~	800030	neurofilament trip
22	167	8.2	1961	Н	A61231	
23	167	8.2	3187	7	JC5837	364K Golgi complex
24	166.5	8.2	1940	Н	A24922	myosin heavy chain
25	166.5	8.2	1999	М	S21801	myosin heavy chain
26	166	8.2	895	N	T45738	tical
27	166	8.2	944	N	S26710	
28	LO.	8.2	1938	٦	JX0178	myosin heavy chain
29	165.5	8.2	1940	٦	804090	myosin heavy chain

myosin heavy chain	trichohyalin - hum	myosin heavy chain	myosin heavy chain	hypothetical prote	skeletal myosin -	hypothetical coile	myosin heavy chain	neurofilament medi	hypothetical prote	involucrin - white	neurofilament trip	myosin II heavy ch	hypothetical prote	myosin heavy chain	hypothetical prote
A23767	A45973	A47297	A33977	T24635	A59294	T38077	A29320	150479	T22976	136930	A27864	S61477	T46146	539083	E71606
~	Н	~	٦	7	~	~	0	7	7	Н	~	N	~	~	7
876	1898	1992	1959	1138	1957	1957	1940	798	1133	428	916	2057	447	936	980
8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.0	8.0	7.9	7.9	7.9	7.9	7.9	7.9	7.9
165	165	165	164.5	164	163.5	163.5	163	162.5	161	160.5	160.5	160.5	160	160	160
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 A59236 embryonic muscle myosin heavy chain - sea squirt (Halocy C;Species: Halocynthia roretzi C;Species: 19-May-2000 #sequence_revision 19-May-2000 #text	K;Arakı, 1.
---------------------------------------------------------------------------------------------------------------------------------------------------------------------	-------------

98: Halocynthia roretzi 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004

submitted to GenBank, February 1999
A,Reference number: A59236
A,Accession: A59236
A,Statuss; preliminary, not compared with conceptual translation
A,Molecule type: mRNA
A,Residues: 1-1927 <ARA>

A; Residues: 1-1927 <ARA>
A; Residues: 1-1927 <ARA>
A; Cross-references: UNIPROT:Q25142; GB:D45163; NID:g1197167; PIDN:BAA08111.1; PID:g11971
A; Cross-references: UNIPROT:Q25142; GB:D45163; NID:g1197167; PIDN:BAA08111.1; PID:g11971
B; Rexperimental source: clone lib lambda gt11; dev stage tailbud embryo
C; Genetics:
A; Gene: MHCemb
C; Superfamily: myosin heavy chain; myosin motor domain homology
F; 89-766/Domain: myosin motor domain homology <AMO>

Length 1927;

13; Indels 111; 9.9%; Score 200.5; DB 2; 23.1%; Pred. No. 0.0082; ve 57; Mismatches 151; 40 DLQTRIMELEGRVRRAAAERGAVELKKNEFQGELE---Query Match
Best Local Similarity 23.1*
Matches 96; Conservative ઠે

---KOREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKTLQRNYG 131 75 ద ò

| :| | ::| || ::| || || 1230 DLAANVESITKAKLNYEKMARNLEEQFSESKTKCDNFCKEVNEL-------NAA 1276 132 RLQQDV-----LQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAV 184 셤 ò

요

:| ||| : :|| || : : 1277 KARFASENGELSRQL----EEREHLMA--------QLTRTKONSSSQQIEE 1314 185 ASRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSEVVLD 244 ઠે 셤

1315 LKRVVE-EETKAKAALAHSVQASRHDNDLLREQYEEEQEA-------KAELQRA 1360 245 SKRQVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAA 304 셤 ઠે

LSVS-----AGEGRNQQK 343

305

ð

LRGE-DDYNMDENEAESETDKQAALAGNDRNID-VFNVEDQKRDTINL-LDQREK 395 344 용 ઠ્ઠ

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A; Molecule type: DNA
A; Residues: 1-61, 'EMNVIQ', 65-376,'V',378-1963 <KAR>
A; Cross-references: GB:J01050; NID:g156399; PIDN:AAA28124.1; PID:g156400
R; McLachlan, A.D.; Karn, J.
Nature 299, 226-231, 1982
Nature 299, PATICLE: Periodic charge distributions in the myosin rod amino acid sequence match cross A; Reference number: A93287; MUID:82272395; PMID:7202124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 847-1333, 'R',1335-1876,'L',1878-1963 <MCL>
A; Residues: 847-1333, 'R',1335-1876,'L', 1878-1963 <MCL>
R; Wills, N.; Gesteland, R.F.; Karn, J.; Barnett, L.; Bolten, S.; Waterston, R.H.
Cell 33, 575-583, 1983
A; Title: The genes sup-7 X and sup-5 III of Caenorhabditis elegans suppress amber nonsen:
A; Reference number: A21074; MUID:83232892; PMID:6571695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 1
A; Map position: 1
A; Alutrons: 21/3; 111/3; 264/1; 525/3; 951/2; 1747/3; 1819/3; 1894/3
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle coiled coil; hydrolase; methylated amino acid; muscle coiled. The coiled coil; hydrolase; methylated amino acid; muscle p; 648-776-780, motoleocide-binding motif A; (P-loop)
F; 662-684/Region: actin binding #status predicted
F; 848-1965/Domain: actin binding #status predicted
F; 848-1965/Domain: coiled coil #status predicted <COI>
                                                                                                                                                                                                                                                                                         myosin heavy ch
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A;Residues: 1873-1963 <WI3>
A;Cross_references: GB:V01494; GB:J01049; NID:g6783; PIDN:CAA24738.1; PID:g6784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1178 AELAKLRRDLEEANMNHENQLGGLRKKHTDAVAELTDÖLDQLNKAKAKVEKDKAQAVRDA 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LIRVLQDQLKTLQRNYGRLQQDVLQFQKNQ 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 TNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRDLSENNDQRQQLQALSE 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 PQPRLQAAG---LPHTEVPQGKGNVLGNSKSQTPAPSSEVVLDSKRQVEKEETNEIQVVN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----QVQAAL-SVSQENPEMEGPERDQLV--IPDGQEEEQEAAGEGRNQQKLRGEDDYNM 352
                                                                                                                             PIDN:CAB05505.1; GSPDB:GN00019; CESP:F11C3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 DLQTRIMELEGRVRRAAAERGAVELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQ
                                                        A;Residues: 1-1963 <W12>
A;Cross-references: BMBL:283107; PIDN:CAB05505.1; GSPDB:GN00019; CESP:Fll:A;Experimental source: clone F32A7
A;Experimental source: clone F32A7
B;Karn, J.; Brenner, S.; Barnett, L.
Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983
A;Title: Protein structural domains in the Caenorhabditis elegans unc-54 th A;Reference number: A3958; MUID:83273600; PMID:6576334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fil63-1963/Region: light meromyosin
Fil28/Modified site: NG,NG,NG-trimethyllysine (Lys) #status predicted
Fil80/Binding site: ATP (Lys) #status predicted
Fi)702,712/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEPORDRLPQEPGREQVVEDRPV-
from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A21074
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                                                                                                            C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R; Du, Z: Leimbac, D.
Submitted to the EMBL Data Library, February 1996
A; December: 220720
A; Reference number: 220720
A; Reference number: 220720
A; Reference number: 220720
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1974 *DUZ>
A; Residues: 1-1974 *DUZ>
A; Coss-references: UNIPROT: Q21000; EMBL: U50309; PIDN: AAB37057.1; GSPDB: GN00023; CESP:F5
A; Coss-references: UNIPROT: Q21000; EMBL: U50309; PIDN: AAB37057.1; GSPDB: GN00023; CESP:F5
A; Genetics:
C; Superfamily: myosin heavy chain; myosin motor domain homology
F; 84-776/Domain: myosin motor domain homology *MMO>
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NyContains: myosin ATPase (EC 3.6.4.1)
CySpecies Caenorhabditis elegans
CySpecies CyTO70; T21629; A93958; A93287; A21074; A02992
CyAccession: T20770; T21629; A93958; A93287; A21074; A02992
Sykeraha, J.
Sykeraha, J.
Sykeraha, J.
Sykeraha, J.
Sykeraha, J.
Sykeraha, CyTO70
A;Reference number: Z19322
A;Residues translated from GB/EMBL/DDBJ
A;Residues: L-1963 vMIL>
A;Residues: L-1963 vMIL>
A;Residues: L-1963 vMIL>
A;Experimental source: clone F11C3
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ADRANSIASSLEKKQKGFDKVLDEWRRKCEALVAEVEQSQRET 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.3%; Pred. No. 0.054;
tive 75; Mismatches 144; Indels
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                                                                                      Caenorhabditis elegans
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Matches 90; Conservative
                                                                                      hypothetical protein F58G4.1
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EMBL: Z49888; PIDN: CAA90064.1; GSPDB: GN00028; CESP: FA
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C;Species: Dictyostellum discoideum
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14867
R;Kivero, F.J.; Kuspa, A.; Brokamp, R.; Matzner, M.; Noegel, A.A.
J. Cell Biol. 142, 735-750, 1998
A;Title: Interaptin, an actin-binding protein of the alpha-actinin superfamily in Dictyc
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A;Cross-references: UNIPROT:076329; EMBL:AF057019; NID:g3549260; PID:g3549261; PIDN:AAC3
                                                                                                                                                                                                                                        A;Introns: 36/3; 72/3; 147/2; 228/3; 261/2; 320/2; 847/3; 881/1; 1317/2; 1500/3; 1653/2,
                                                                                                                                                                                                                                                                                                                                                                                                                           2676 ERIQKELEDKVRREKEEAARQEKERQEQ-EARMRE----AREAELSRORMEQQRRSQQNP 2730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 DORQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNSKSQTPAPSSEVVLDSKRQVEKEE 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2731 YMNQQGQYSQQPPPSYQQSSYPNNYQPGQQGNQPPNYQQ----PSHQSMQQGHQAGYQQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 QKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRDLSE-----nn
                                                                                                                                                                                                                                                                                                                                                                                     37 RSVDLQTRIMELEGR-----VRRA-----AAERGAVELKKNEFQGELEKQREQL
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                                                                                                                                                                                                                                                                                     ; Score 176; DB 2; Length 3498;
; Pred. No. 0.32;
67; Mismatches 147; Indels 8
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A; Accession: T14867
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20.0%; Pred. No. 0.17;
ive 89; Mismatches 156;
                    A,Accession: T22330
A,Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: DNA
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                                                            A;Molecule type: DNA
A;Residues: 1-3498 <WIL>
A;Cross-references: UNIPROT:Q20497;
A;Experimental source: clone F47A4
                                                                                                                                                                                                                                                                                        8.7%;
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 21.8<sup>3</sup>
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
A; Reference number: Z19549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: abpD
A;Introns: 173/2; 1680/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2645 MRIQR----
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                                                                                                                                                                                        A, Gene: CESP: F47A4.2
A, Map position: X
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                                                                                                                                                                         chromosome segregation protein smcl - Synechocystis sp. (strain PCC 6803)
C, Species: Synechocystis sp.
C, Species: Synechocystis sp.
A; Variety: PCC 6803
C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: S77524
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis S.
A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S77524
A; Accession: S77524
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-1200 «KAN»
A; Residues: 1-1200 «KAN»
A; Residues: 1-1200 «KAN»
A; Residues: 1-1200 «KAN»
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Superfamily: chromosome segregation protein SMC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|:|
396 -QAIASASEAWVQEQTQLSRTVNQLQDELIPQRSQLAQLEERQQQLLTNLAELTPLLTKV 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVELEEKQFAQGQFNFQGEALTSQ1QTLA-SDLAQLEQERSLLQETQTRLLKEQQEKQRQ 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -DRLPQEPGREQVVE-----DRPVGGRGFGG-AGELGQT-PQVQAALSVSQENP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMEGPERDQLVIPDGQEEQGEAGG-----EGRNQ----QKLRGEDDYNMDENEAESE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --AGGRIGFLVVED---DGVAAAGIEILKQAKAGRATFLPLNKIRPPKGQNPNLSYAHGY 620
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22330
R;Mortimore, B.
submitted to the EMBL Data Library, June 1995
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BLERTLERLAADRQKAEKYQALRQQVQEKQGWAKVIQYKAVEQQRQKLWGQLERDREQSQ
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                                             ---KLYQDEKAVLVNNITTGERLIRVLQD---
                 DENEAESETDKQAALAGNDRNI - - - - DVFNVEDQKRDTINLLDQREKRNHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%; Score 176; DB 2; Length 1200; ilarity 22.8%; Pred. No. 0.088; Conservative 70; Mismatches 146; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SRDLSENND----QRQQLQALSEPQPRL-
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Matches 100; Conserv
                                                               1463
                 353
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us-10-759-803-2.rpr

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A;Residues: 1-1164 <WIL>
A;Cross-references: UNIPROT:P92021; EMBL:Z81118; PIDN:CAB03330.1; GSPDB:GN00023; CESP:T1
A;Experimental source: clone T10G3
                                                                                                                                                                                                                                                              | |: :||: |: :|| 325 LSSITAKLEDEQVVVLKH----QRQIKELQARIEELEEEVEAERQARAKAEKQRADLARE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                    187 RDLSENNDGRQQLQALSEPQPRLQ-----AAGLPH---------TEVP 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QCKGNVLGNSKSQTPAPSSEVVLDSK----RQVEKEETN-----EIQVVNEEPQRDRLP 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 QEPGREQVVEDRPVGGRGPGGAGELGQTPQVQAALSVSQENPEMEGPERDQLVIPDGQEE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            558 DEESRER------ATLLIGKFRNLEHDLDNLREQVEEEAEGKADL-----QRQ 598
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                                                                                                                                                                                                                               41 LQTRIMELEGRVRRAAAERGAVELKKNEFQG------ELEKQREQLDKIQSSHNFQ 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T10G3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440 -EMAEGVDÓLNKLKAKAEKEKNEYYGOLNDLRAGVDHITNEKAAQEKIAKOLOHTLNEV-
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                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: 5
A;Introns: 15/3; 73/3; 387/3; 412/3; 708/3; 818/3; 894/3; 982/3; 1080/2
                                                                                                                                                                                96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 172; DB 2; Length 1201;
Pred. No. 0.14;
; Mismatches 155; Indels 96
A;Gene: FlyBase:Mhc
A;Crosa-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.5%; Score 171.5; DB 2;
19.6%; Pred. No. 0.15;
ative 80; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Riburton, J. submitted to the EMBL Data Library, October 1996 A;Reference number: 219937 A;Accession: 124806 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                           ch 8.5%; Scoll Similarity 20.6%; Pre 84; Conservative 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 87; Conserv
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                                                                                                                              Query Match
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                                                                                                                                                        Best Local
Matches 8
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                                       D35815

myosin heavy chain 4, muscle - fruit fly (Drosophila melanogaster) (fragment)

C; Species Drosophila melanogaster
C; Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: D35815

R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A;Recession: D35815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1175 <COL>
A;COLS-references: UNIPROT: Q9TY21; EMBL: X53155
A;Coss-references: UNIPROT: Q9TY21; EMBL: X53155
A;Coss-references: UNIPROT: Q9TY21; EMBL: X53155
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
A;Genetics:
C;Genetics:
C;Genetics:
A;Coss-references: RlyBase: FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
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C;Species: Drosophila melanogaster
C;Species: Brar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: B35815
R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A;Reference number: A35815; MUID:90346288; PMID:2116987
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A;Molecule type: DNA
A;Residues: 1-1201 <COL>
A;Coss-references: UNIPROT:018392; EMBL:X53155; NID:g8219; PIDN:CAA37311.1; PID:g254693
A;Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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LSSITAKLEDEQVVVLKH----QRQIKELQARIBELEEEVEAERQARAKAEKQRADLARE
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Best Local Similarity 20.6%; Pred. No. 0.14;
Matches 84; Conservative 73; Mismatches 155; Indels
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Qy 308SQENPEMECPERDQLVIPDGQEEEQBAAGEGRNQQKLRGEDDYN 351	Qy 352 MDENEAESETDKQAALAGNDRNIDVENVEDQKRDTINLLDQREKRNHT 399 ::: ::	RESULT 13 A59287 myosin heavy chain - fluke (Schistosoma mansoni) (strain Brazilian LE)	C;Species: Schistosoma mansoni C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004 C;Accession: A59287 R;Weston, D.S.; Schmitz, J.; Kemp, M.; Kunz, W.	Mol. Biochem. Parasitol. 58, 161-164, 1993  A;Title: Cloning and sequence characterization of a complete myosin heavy chain cDNI A;Reference number: A59287; MUID:93211444; PMID:8459827	A, A.C.C.B.1101. A.J.S.L. B. D. Compared with conceptual translation A, Rolecule type: mRNA A, Residues: 1.1940 «WES. A, Cross-references: UNIPROT:002456; GB:L01634; PIDN:AAA29905.1	A,Experimental source: strain Brazilian LE C,Genetics: A,Gene: MYH	C;Superfamily: myosin heavy chain; myosin motor domain nomology F;82-752/Domain: myosin motor domain homology <mmo></mmo>	89 80	QY 41 LQTRIMELEGRVRRAABERGAVELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQD 100	δ	138LOFORNQTHLERKFSYDLSQCINQMKEVKEQCEERLEEVTKKGNEAVASRDL	DD 1132 VVDRLEEQDGATAAQSDLIXKKEAELMKLKKULEDIRLUQNEQATAIMKKNQSDALNEL 1189  QY 190 SENNDQRQQLQALSEPQPRLQAAGLPHTEV	Db	1250 DEATRNLNEQA 280 EDRPVGGRGFGGA ::		1345	DB 1405 AKLIÇGELEDLIMVDVEKANGLIMDÇIERNÇINKTIN 1459 RESULT 14	myosin heavy chain 1, muscle - fruit fly (Drosophila melanogaster)
171 ERIEEVTKKGNEAVASRDLSENNDQRQQLQALSEPQPRLQAAGLPHTEVPQGKGNVLGNS 230	KSQTPAPSSEVVLDSKRQVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFG ::::::  ::  ::  :::	291 GAGELGQTPQVQAALSVSQENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQ 342	343 KLRGEDDYNMDENEAESETDKQAALAGNDRNIDVFNVEDQKR 384   :	385DTINLLDQREKRNHTL 400		uscle - scallop (Aequipecten ir	C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004 C;Accession: A40997; S13557	R;Nyitray, L.; Goodwin, E.B.; Szent-Gyoergyi, A.G. J. Biol. Chem. 266, 18469-18476, 1991 A;Title: Complete primary structure of a scallop striated muscle myosin heavy chain A;Reference number: A40997; MUID:92011595; PMID:1917970	cession: A40'37/ lecule type: mRNA sidues: 1-1938 <nxi> oss-references: UNIPROT:P24733; GB:X55714; NID:q5611; PIDN:CAA39247.1; PID:q5612</nxi>	oerfamily: myosin heavy chain; myosin motor domain homology words: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide -763/Domain: myosin motor domain homology cMMOT> 5-183/Region: nucleotide-binding motif A (P-loop)	in binding #status predi in binding #status predi iled coil #status predic	;836-1276.Region: S2 ;1277-1938/Region: light meromyosin ;182/Binding site: ATP (Lys) #status predicted ;693,703/Active site: Cys #status predicted	larity 2 Conservati	DLOTRIMELEGRVERAAABERGAVELKKNEFGGELEKQREQLDKIQSSHNFQLESVNKLYQ 99 	100 DEKAVLVNNITTGERLIRVLQDQLKTLQRNYGRLQQDVLQFQKNQ 144	145 TNLERKFSYDLSQCINQ-MKEVKEQCEERIEEVTKKGNEAVASRDLSENNDOR 196 	197 QOLQALSEPQPRLQAAGLPHTEVPQCKGNVLGNSKSQTPAPSSEVVLDSKRQVEKEETNE 256 11	257 IQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSV 307

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F;227-234/Region: nucleotide-binding motif A (P-loop)
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R;George, E.L.; Ober, M.B.; Emerson Jr., C.P.
Mol. Cell. Biol. 9, 2957-2974, 1989
A;Title: Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gen
A;Reference number: A32491; MUID:89384556; PMID:2506434
A;Reference number: A32491; MUID:89384556; PMID:2506434
A;Reference number: A32491; MUID:89384556; PMID:2506434
A;Reference number: A32491
A;Reference number: A32491; MUID:89384556; PMID:2506434
A;Reference number: A32491
A;Reference number: A32491
A;Reference number: CGEDO
A;Cross-references: UNPROT:P05661; GB:M61229; GB:M27194
A;Rote: the authors translated the codon TGC for residue 329 as Ser
C;Genetics:
A;Gene: FlyBase:MC
A;Cross-references: FlyBase:FBgn0002741
C;Genetics:
A;Gene: FlyBase:Mc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain: myosin motor domain homology
C;Reywords: AFP; nucleotide binding; P-loop
F;137-1032/Pomain: myosin motor domain homology #status atypical <MMO>
F;227-234/Region: nucleotide-binding motif A (P-loop)
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C;Species: Drosophila melanogaster
C;Species: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B32491
R;George, E.L.; Ober, M.B.; Emerson Jr., C.P.
Mol. Cell. Biol. 9, 2957-2974, 1989
A;Title: Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gen
A;Reference number: A32491; MUID:89384556; PMID:2506434
A;Accession: B32491
A;Accession: B32491
A;Residues: 1-2411 cGEO-A;Accession: GEO-A;Cross-references: UNIPROT:P05661; GB:M61229; GB:M27194
A;Rosidues: 1-2411 cGEO-A;Cross-references: UNIPROT:P05661; GB:M61229; GB:M27194
A;Rosidues: FlyBase:Mhc
A;Gene: FlyBase:Mhc
A;Gene: FlyBase:Mhc
C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP; nucleotide binding; P-loop
F;137-1032/Domain: myosin motor domain homology #status atypical cMMO>
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1449 LEQTLDELEDSLEREKKVRGDVEKSKRKVEGDLKLTQEAVADLERNKKELEQTIQRKDKE 1508
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1 Similarity 20.9%; Pred. No. 0.41;
86; Conservative 77; Mismatches 148; Indels 100;
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1449 LEQTLDELEDSLEREKKVRGDVEKSKRKVEGDLKLTQEAVADLERNKKELEQTIQRKDKR 1508
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      8.4%; Score 1/v, __ 20.9%; Pred. No. 0.42; arive 77; Mismatches 148; Indels 100; __ reversol.DKIC
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Query Match
Best Local Similarity 20.9%
Matches 86; Conservative
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